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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:56:54 ; Search time 79.2611 Seconds
(without alignments)
4199.299 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	5882	99.3	1178	3	AA71311	Aay71311 Human neu
2	5815	98.2	1192	4	AAU04591	Aau04591 Human Nog
3	5815	98.2	1192	5	ABP68600	Abp68600 Human pan
4	5815	98.2	1192	6	ABR59667	Abr59667 Human Nog
5	5810	98.1	1192	3	AA56967	Aay56967 Human MAG
6	5810	98.1	1192	4	AAB82349	Aab82349 Human NOG
7	5810	98.1	1192	5	ABG30938	Abg30938 Human Nog
8	5810	98.1	1192	5	ABB81078	Abb81078 Human neu
9	5526.5	93.3	1246	4	AAU33228	Aau33228 Novel hum

10	4560	77.0	983	6	ABU11573	Abu11573	Human MDD
11	4400	74.3	893	3	AAy95012	Aay95012	Human sec
12	4296.5	72.5	1163	3	AAy71310	Aay71310	Rat neuri
13	4296.5	72.5	1163	5	ABB81074	Abb81074	Rat neuro
14	4294.5	72.5	1162	3	AAy71557	Aay71557	Rat Nogo
15	4286.5	72.4	1163	3	AAy71384	Aay71384	Alternati
16	3388.5	57.2	974	3	AAy71560	Aay71560	Rat Nogo
17	3146.5	53.1	642	2	AAW58383	Aaw58383	Human sec
18	3146.5	53.1	642	4	AAB90682	Aab90682	Human BG1
19	2715	45.8	803	3	AAy71562	Aay71562	Rat Nogo
20	2529.5	42.7	737	3	AAy71386	Aay71386	Rat Nogo
21	2487.5	42.0	746	3	AAy71391	Aay71391	Rat Nogo
22	2457	41.5	736	3	AAy71398	Aay71398	Rat Nogo
23	2449.5	41.4	732	3	AAy71399	Aay71399	Rat Nogo
24	2405.5	40.6	695	3	AAy71387	Aay71387	Rat Nogo
25	2344.5	39.6	684	3	AAy71394	Aay71394	Rat Nogo
26	1948.5	32.9	552	3	AAy71388	Aay71388	Rat Nogo
27	1743	29.4	502	3	AAy71396	Aay71396	Rat Nogo
28	1634.5	27.6	475	3	AAy71389	Aay71389	Rat Nogo
29	1566.5	26.4	403	3	AAy71563	Aay71563	Rat Nogo
30	1552.5	26.2	457	3	AAy71392	Aay71392	Rat Nogo
31	1495.5	25.2	373	3	AAy53624	Aay53624	A bone ma
32	1495.5	25.2	373	3	AAy56969	Aay56969	Human MAG
33	1495.5	25.2	373	3	AAB24242	Aab24242	Human Nog
34	1495.5	25.2	373	4	AAB82350	Aab82350	Human NOG
35	1495.5	25.2	373	5	AAM47954	Aam47954	Human RTN
36	1495.5	25.2	373	5	ABP68601	Abp68601	Human pan
37	1495.5	25.2	373	5	ABB81079	Abb81079	Human neu
38	1487.5	25.1	373	5	ABG30937	Abg30937	Human Nog
39	1412	23.8	289	3	AAy56968	Aay56968	Human MAG
40	1327	22.4	284	3	AAy95030	Aay95030	Human clo
41	1264	21.3	356	3	AAy71390	Aay71390	Rat Nogo
42	1225.5	20.7	379	7	ADB85283	Adb85283	Rat fooce
43	1205.5	20.4	374	3	AAy71397	Aay71397	Rat Nogo
44	1196.5	20.2	361	3	AAy71385	Aay71385	Alternati
45	1189	20.1	359	3	AAy71558	Aay71558	Rat Nogo

ALIGNMENTS

RESULT 1

AAy71311

ID AAY71311 standard; protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 187
FT /label= Unknown
FT Misc-difference 188
FT /label= Unknown
FT Misc-difference 189
FT /label= Unknown
FT Misc-difference 190
FT /label= Unknown
FT Misc-difference 221
FT /label= Unknown
FT Misc-difference 328
FT /label= Unknown
FT Misc-difference 477
FT /label= Unknown
FT Region 977. .1012
FT /note= "Region specifically described in claim 16"
FT Region 994. .1174
FT /note= "Region specifically described in claim 16"
FT Region 1079. .1114
FT /note= "Region specifically described in claim 16"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 11; Fig 13; 122pp; English.
XX
CC The present sequence is a human Nogo protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The human Nogo
CC sequence was derived by aligning human expressed sequence tags (ESTs)
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments
CC displaying neurite growth inhibitory activity are used in the treatment
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.

CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers

XX

SQ Sequence 1178 AA;

Query Match 99.3%; Score 5882; DB 3; Length 1178;
Best Local Similarity 99.7%; Pred. No. 5.4e-296;
Matches 1175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Db	1	MEDLDQSPLVSSSDSVPRPQPAFKYQFVREPED	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSS	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSS	120
Qy	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Db	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAA	240
Db	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAA	240
Qy	241	LSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGS	300
Db	241	LSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGS	300
Qy	301	IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALT	360
Db	301	IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALT	360
Qy	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDK	420
Db	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDK	420
Qy	421	EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE	480
Db	421	EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE	480
Qy	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVANMPEGLTPDL	540
Db	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVANMPEGLTPDL	540
Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTS	600

Db	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSIGKE	660
Db	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSIGKE	660
Qy	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV	720
Db	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV	720
Qy	721	EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Db	721	EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Db	781	GKPYLESFKLSLVNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Qy	841	TETFSDDSSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	841	TETFSDDSSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLPPDVSA LGHTQAEIESIVKPKVLE	960
Db	901	PHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLPPDVSA LGHTQAEIESIVKPKVLE	960
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	1021	SIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178

RESULT 2

AAU04591

ID AAU04591 standard; protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;
 KW Krabbe's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1054. .1119
 FT /label= Lumenal_extracellular_domain
 FT /note= "This sequence is specifically claimed"
 FT Peptide 1055. .1094
 FT /label= Pep1
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1064. .1088
 FT /label= Pep2
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1074. .1098
 FT /label= Pep3
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1084. .1108
 FT /label= Pep4
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1095. .1119
 FT /label= Pep5
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 XX
 PN WO200151520-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001041.
 XX
 PR 12-JAN-2000; 2000US-0175707P.
 PR 26-MAY-2000; 2000US-0207366P.
 PR 29-SEP-2000; 2000US-0236378P.
 XX
 PA (UYYA) UNIV YALE.
 XX
 PI Strittmatter SM;
 XX
 DR WPI; 2001-442138/47.
 DR N-PSDB; AAS09453.
 XX
 PT Novel Nogo receptor protein useful for identifying modulator of Nogo
 PT protein or Nogo receptor protein, which is useful for treating central
 PT nervous system disorders.
 XX
 PS Example 1; Page 101-104; 109pp; English.
 XX
 CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon

CC growth inhibitor. The invention relates to the use of the nogo receptor,
CC nogo protein, their nucleic acids, vectors expressing them and antibodies .
CC against them, to isolate agents which block nogo receptor mediated axonal
CC growth. The agent is useful for treating a central nervous system
CC disorder which is a result of cranial or cerebral trauma, spinal cord
CC injury, stroke or a demyelinating disease selected from multiple
CC sclerosis, monophasis demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC Spongy degeneration, Alexander's disease, Canavan's disease,
CC metachromatic leukodystrophy, viral infection and Krabbe's disease

XX

SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 4; Length 1192;
Best Local Similarity 97.2%; Pred. No. 1.6e-292;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSLSP	226
		: : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF	600

Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAELGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 3

ABP68600

ID ABP68600 standard; protein; 1192 AA.

XX

AC ABP68600;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed protein SEQ ID NO 71.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US002781.
 XX
 PR 30-JAN-2001; 2001US-0265305P.
 PR 31-JAN-2001; 2001US-0265682P.
 PR 09-FEB-2001; 2001US-0267568P.
 PR 21-MAR-2001; 2001US-0278651P.
 PR 28-APR-2001; 2001US-0287112P.
 PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI; 2002-627435/67.
 DR N-PSDB; ABV94680.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 5; Length 1192;
 Best Local Similarity 97.2%; Pred. No. 1.6e-292;
 Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKESQAQIRETETFSDDSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKESQAQIRETETFSDDSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGH	945

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|||||
Db      901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAALA- 959
Qy      946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGV 1005
|||||
Db      960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019
Qy      1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
|||||
Db      1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
Qy      1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
|||||
Db      1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
Qy      1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
|||||
Db      1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

```

RESULT 4

ABR59667

ID ABR59667 standard; protein; 1192 AA.

XX

AC ABR59667;

XX

DT 22-JUL-2003 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
KW demyelinating disease; multiple sclerosis; monophasic demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

XX

OS Homo sapiens.

XX

PN WO2003031462-A2.

XX

PD 17-APR-2003.

XX

PF 04-OCT-2002; 2002WO-US032007.

XX

PR 06-OCT-2001; 2001US-00972599.

XX

PA (UYYA) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2003-393433/37.

DR N-PSDB; ACC81048.

XX

PT New human Nogo receptor polypeptides and nucleic acids, useful for
PT decreasing inhibition of axonal growth by a central nervous system
PT neuron, or in treating central nervous system disease, disorder or
PT injury, e.g. spinal cord injury.

XX
PS Disclosure; Page 131-135; 148pp; English.

XX
CC The invention relates to a novel nucleic acid encoding a polypeptide
CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
CC 1-20 conservative amino acid substitutions, and less than a complete CTS
CC domain, provided that a partial CTS domain, if present, consists of no
CC more than the first 39 consecutive residues. The nucleic acid of the
CC invention has neuroprotective activity. The polynucleotide may have a use
CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
CC axonal growth by a central nervous system (CNS) neuron. The NgR
CC polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-
CC dependent signal transduction in the central nervous system neuron may be
CC used in treating central nervous system disease, disorder or injury, e.g.
CC spinal cord injury. Expression of an NgR protein may be associated with
CC inhibition of axonal regeneration following cranial, cerebral or spinal
CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
CC monophasic demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
CC sequence is used in the exemplification of the invention

XX
SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 6; Length 1192;
Best Local Similarity 97.2%; Pred. No. 1.6e-292;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
|
Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP 120
|
Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP 120

Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
|
Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy 181 SSGA-----VXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
| : : |
Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
|
Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy 287 GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV 346
|
Db 301 GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

Qy 347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
|
Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy 407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466

Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSF SKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSF SKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSA DLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 5

AA56967

ID AAY56967 standard; protein; 1192 AA.

XX

AC AAY56967;

XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human MAGI polypeptide.
 XX
 KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
 KW psychiatric disorder; developmental disorder; inflammatory disorder;
 KW stroke; cytostatic; cerebroprotective; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200005364-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-GB002360.
 XX
 PR 22-JUL-1998; 98GB-00016024.
 PR 19-JUL-1999; 99GB-00016898.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Michalovich D, Prinjha RK;
 XX
 DR WPI; 2000-182693/16.
 DR N-PSDB; AAZ56886.
 XX
 PT Novel polypeptides related to neuroendocrine-specific proteins and
 PT polynucleotides useful for diagnosis of various diseases and for
 PT treatment of cancer and neurological disorders.
 XX
 PS Claim 2; Page 20-21; 35pp; English.
 XX
 CC The invention relates to human MAGI protein, which is similar to
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
 CC and antibodies are useful for treating diseases, including neuropathies,
 CC spinal injury, neuronal degeneration, neuromuscular disorders,
 CC psychiatric disorders and developmental disorders, cancer, stroke and
 CC inflammatory disorders. The polynucleoitde is also useful for chromosome
 CC localization and for tissue expression studies. The present sequence
 CC represents the human MAGI protein
 XX
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 3; Length 1192;
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120

Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSOSSPIEIIIDEFPTLISSKTDSESKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSOSSPIEIIIDEFPTLISSKTDSESKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA-	959

Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE	1192

The present sequence is that of human NOGO-A. NOGO-A is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel splice variant, NOGO-C (see AAB82348). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels

SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 4; Length 1192;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

[illegible][illegible]

Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180

Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
|||: | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNINLHXQQELPTALTCLVKEDVV 346
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 347 SSEKAKDSFNEKRAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406

[illegible]

Qy 467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTQVTE 526

Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586

Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETTFSDSSPIEIIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETTFSDSSPIEIIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAIGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAI-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 7

ABG30938

ID ABG30938 standard; protein; 1192 AA.

XX

AC ABG30938;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;

KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;

KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;

KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200257483-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 18-JAN-2002; 2002WO-GB000228.
 XX
 PR 18-JAN-2001; 2001GB-00001312.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
 XX
 DR WPI; 2002-599722/64.
 DR N-PSDB; ABK90134.
 XX
 PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides.
 XX
 PS Disclosure; Page 59-62; 68pp; English.
 XX
 CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent
 CC is a modulator of Nogo or BACE activity. The method is useful in treating
 CC acute neuronal injuries, such as spinal or head injury, stroke,
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
 CC hypertrophy) of the central nervous system. The BACE polypeptide is
 CC useful in screening methods to identify agents that may act as modulators
 CC of BACE activity and in particular agents that may be useful in treating
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
 CC and the polynucleotide encoding the BACE polypeptide are useful in
 CC manufacturing a medicament for the treatment or prevention of disorders
 CC responsive to the modulation of Nogo activity, in alleviating the
 CC symptoms or improving the condition of a patient suffering from this
 CC disorder, in axon regeneration, or in preventing metastasis or spreading
 CC of a cancer. The polynucleotide may also be an essential component in
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy
 CC techniques. The present amino acid sequence represents the human NogoA
 CC protein of the invention
 XX
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 5; Length 1192;
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885

Db	841		SNDDLFI	SKEAQI	RETET	TFSDSS	PIEI	I	DEFPT	LISSKT	DSFSKL	AREYTD	LLEVSHK	SEI	900
Qy	886		ANAPDG	GAGSLP	CTELPH	DL	SLKNIQ	PKVEEK	ISFSDD	FSKNGS	SATSKV	LLLLPP	DV	SALGH	945
Db	901		ANAPDG	GAGSLP	CTELPH	DL	SLKNIQ	PKVEEK	ISFSDD	FSKNGS	SATSKV	LLLLPP	DV	SALA-	959
Qy	946		TQAEIES	IVKPKV	LEKEAE	KKLPSD	TEKEDR	SPSAIF	SADLGK	TSVVDL	LYWRDI	KK	TGV	1005	
Db	960		TQAEIES	IVKPKV	LVKEAE	KKLPSD	TEKEDR	SPSAIF	SAELSK	TSVVDL	LYWRDI	KK	TGV	1019	
Qy	1006		VFGASL	FLLLSL	TVFSIV	SVTAYI	ALALLS	VTISFRI	YKGV	IQAIQK	SDEGHP	FRAYLES	1065		
Db	1020		VFGASL	FLLLSL	TVFSIV	SVTAYI	ALALLS	VTISFRI	YKGV	IQAIQK	SDEGHP	FRAYLES	1079		
Qy	1066		EVAISEE	LVQKYS	NSALGH	VNCTIK	ELRRLF	LVDDL	VDSLK	FAVLMW	VFTYV	GALFNGLT	1125		
Db	1080		EVAISEE	LVQKYS	NSALGH	VNCTIK	ELRRLF	LVDDL	VDSLK	FAVLMW	VFTYV	GALFNGLT	1139		
Qy	1126		LLILALI	SLFSVP	VIYERH	QAQIDH	YLG	LANKNV	KDAMAKI	QAKIPGL	KR	KAE	1178		
Db	1140		LLILALI	SLFSVP	VIYERH	QAQIDH	YLG	LANKNV	KDAMAKI	QAKIPGL	KR	KAE	1192		

RESULT 8

ABB81078

ID ABB81078 standard; protein; 1192 AA.

XX

AC ABB81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR N-PSDB; ABN86601.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.
 XX
 PS Example; Page 53-56; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the human
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen
 XX
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 5; Length 1192;
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDDEEEEEEEEEDEDEDLEELEVLERKPA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDDEEEEEEEEEDEDEDLEELEVLERKPA 60
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120
 Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLDGPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005

Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLES 1065
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLES 1079
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 9

AAU33228

ID AAU33228 standard; protein; 1246 AA.

XX

AC AAU33228;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #3719.

XX

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US008656.

XX

PR 18-APR-2000; 2000US-00552929.

PR 26-JAN-2001; 2001US-00770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.

XX

PS Claim 20; Page 737; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 1246 AA;

Query Match 93.3%; Score 5526.5; DB 4; Length 1246;
 Best Local Similarity 93.0%; Pred. No. 1.5e-277;
 Matches 1123; Conservative 13; Mismatches 39; Indels 33; Gaps 10;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Db	42	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	101
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	102	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	161
Qy	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	162	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	221
Qy	181	SSGA-----VXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: : :	
Db	222	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	281
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	282	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	341
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	342	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	401
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	402	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	461
Qy	407	DKKCFADSLEQTNHEKDESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	462	DKKCFADSLEQTNHEKDESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	521
Qy	467	PLLEDPTSENXTDEKKIEEKKAIIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	522	PLLGDPSTSENKTDEKKIEEKKAIIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	581
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSPF	586
Db	582	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSPF	641

Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	642	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	701
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	702	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	761
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	765
Db	762	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	821
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	822	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	881
Qy	826	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	882	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	941
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH	945
Db	942	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA-	1000
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV	1005
Db	1001	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1060
Qy	1006	VFGAS-LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY--	1062
Db	1061	VFGASAVFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAISG	1120
Qy	1063	-LESEVAISEELVQKYSNSALGHV-NCTIKELRR--LFLVDDLVDLSLK-FAVLMWVFTY	1116
		: : : : : :	
Db	1121	NLESCLYLRELGSGRYSNSALGSMWNCTVKGNFRAPSFFSWMDLVDLSLRSFAVLMWVFTY	1180
Qy	1117	VGALFNGLTLL-----ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI	1170
		: :	
Db	1181	VGCL--GLMVLDTTGFWALNFISSSGSWLIYERHQAQIDHYLGLANKNVKDAMAKIQAKI	1238
Qy	1171	PGLKRKAE	1178
Db	1239	PGLKRKAE	1246

RESULT 10

ABU11573

ID ABU11573 standard; protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;

KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX

PD 10-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US009944.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-058431/05.

DR N-PSDB; ABX34563.

XX

PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.

XX

PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.

XX

CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded

Db 699 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-TQAEIES 757

Qy 953 IVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLF 1012
 ||||| : |||||

Db 758 IVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLF 817

Qy 1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 1072
 |||||

Db 818 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 877

Qy 1073 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 1132
 |||||

Db 878 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 937

Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||||

Db 938 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 983

RESULT 11

AA95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
 KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

*PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX

PF 24-AUG-1999; 99WO-US019351.

XX

PR 24-AUG-1998; 98US-0097638P.

PR 24-AUG-1998; 98US-0097659P.

PR 09-SEP-1998; 98US-0099618P.

PR 28-SEP-1998; 98US-0102092P.

PR 25-NOV-1998; 98US-0109978P.

PR 23-DEC-1998; 98US-0113645P.

PR 23-DEC-1998; 98US-0113646P.

PR 23-AUG-1999; 99US-00379246.

XX

PA (ALPH-) ALPHAGENE INC.

XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

XX

PT New secreted or transmembrane proteins and polynucleotides encoding them,
PT useful for treating neurodegenerative disorders, autoimmune diseases and
PT cancer.

XX

PS Claim 73; Page 322-325; 357pp; English.

XX

CC The invention relates to 40 human secreted proteins (AA94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
CC secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
CC activity; cell proliferation; differentiation; immune modulation;
CC haematopoiesis regulation; tissue growth activity; activin/inhibin
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; anti-inflammatory activity; and tumour inhibition activity. The
CC proteins may be administered to patients as vaccines, and the nucleotides
CC may be used as part of a gene therapy regime. Diseases or conditions that
CC may be treated using the proteins or nucleotides of the invention include
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
CC allergic reactions such as asthma and anaemia. They may also be used for
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
CC activity may additionally be useful as contraceptives. Nucleic acid
CC sequences of the invention may be used in chromosome mapping, and as a
CC source of diagnostic primers and probes. The present sequence represents
CC one of the 40 proteins of the invention

XX

SQ Sequence 893 AA;

Query Match 74.3%; Score 4400; DB 3; Length 893;
Best Local Similarity 98.9%; Pred. No. 2e-219;
Matches 884; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

Qy	286	MGSSFSVSPKAESAVIVANPREEIIVKNKDDEEEKLVSNILHXQQELPTALTCLKVKEDEV	345
Db	1	MGSSFSVSPKAESAVIVANPREEIIVKNKDDEEEKLVSNILHNQQELPTALTCLKVKEDEV	60
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESK	405
Db	61	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESK	120
Qy	406	VDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNI	465
Db	121	VDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNI	180
Qy	466	FPLLEDPTSENXTDEKKIEEKKQAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVT	525
Db	181	FPLLDGPTSENKTDEKKIEEKKQAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVT	240
Qy	526	EEVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS	585
Db	241	EEVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS	300

Qy 586 FEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY 645
 |||||
 Db 301 FEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY 360
 |||||
 Qy 646 EEAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYS 704
 |||||
 Db 361 EEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYS 420
 |||||
 Qy 705 EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMLVKESLTETSFESM 764
 |||||
 Db 421 EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMLVKESLTETSFESM 480
 |||||
 Qy 765 IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV 824
 |||||
 Db 481 IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV 540
 |||||
 Qy 825 YSNDDLFIKSEAQIRETETFSDDSPIEIDEFPTLISSKTDSESKLAREYTDLEVSHKSE 884
 |||||
 Db 541 YSNDDLFIKSEAQIRETETFSDDSPIEIDEFPTLISSKTDSESKLAREYTDLEVSHKSE 600
 |||||
 Qy 885 IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALG 944
 |||||
 Db 601 IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA 660
 |||||
 Qy 945 HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAIDLKTSVVDLLYWRDIKKTG 1004
 |||||:|||||
 Db 661 -TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTG 719
 |||||
 Qy 1005 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLE 1064
 |||||
 Db 720 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLE 779
 |||||
 Qy 1065 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGL 1124
 |||||
 Db 780 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGL 839
 |||||
 Qy 1125 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||||
 Db 840 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 893
 |||||

100%
 990-178

RESULT 12

AA71310

ID AAY71310 standard; protein; 1163 AA.

XX

AC AAY71310;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.

XX

OS Rattus sp.

XX

Field	Key	Location/Qualifiers
FT	Inhibitory-site	1. .171
FT		/note= "Inhibits NIH 3T3 fibroblast spreading"
FT	Modified-site	30
FT		/note= "Casein kinase II site"
FT	Region	31. .58
FT		/note= "Acidic region"
FT	Region	31. .57
FT		/note= "Region specifically described in claim 16"
FT	Region	172. .259
FT		/note= "This region is not essential for inhibitory activity"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242. .244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	404
FT		/note= "Encoded by TTG"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468. .470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	488
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Inhibitory-site	542. .722
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Peptide	623. .640
FT		/note= "used as immunogen to generate antibody AS 472"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694. .696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Peptide	762. .1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"

FT Modified-site 863
 FT /note= "Casein kinase II site"
 FT Modified-site 868
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 893
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 912. .914
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 925. .927
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 954
 FT /note= "PKC and casein kinase II sites"
 FT Modified-site 956
 FT /note= "PKC and casein kinase II sites"
 FT Region 975. .1162
 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 976. .1163
 FT /note= "C-terminal common region found in Nogo A, B and C
 FT isoforms"
 FT Domain 988. .1023
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region specifically
 FT described in claim 16"
 FT Modified-site 1024
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1071. .1073
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1073
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1089
 FT /note= "Protein kinase C (PKC) site"
 FT Domain 1090. .1125
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region specifically
 FT described in claim 16"
 FT Modified-site 1141. .1143
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1143
 FT /note= "Protein kinase C (PKC) site"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 DR N-PSDB; AAD01173.
 XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 3; Fig 2A; 122pp; English.

XX

CC The present sequence is a rat Nogo A protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The protein was
CC derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated
CC from hexanucleotides-primed rat brain stem/spinal cord library, and Olil8
CC cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins
CC and fragments displaying neurite growth inhibitory activity are used in
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 3; Length 1163;
Best Local Similarity 74.0%; Pred. No. 6.2e-214;
Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
| | | : | | | | | | | | | | | | | | | | | | : | | : | | | | | | | | |
Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEDDEEEEDDEDEDLEELEVLERK 60

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118
| | | | | | | | | | | | | | | | | | | | | | : | | : |
Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKR 178
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 167 RGSGSVDETLFALPAASEVPVPSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
| | | | | | | | | | | | : | | : | : | | | | : | : | : | | | | | | | |

Db 227 SPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286

Qy 285 EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE 344
 ||||| ||| |||::| | :||:|::|::|: || : || || | |||

Db 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340

Qy 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403
 ||| || | ||| ::| ||:|||||||: ||||: | | |:| | :|:

Db 341 VVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE 396

Qy 404 SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463
 ||||:| | |||| : ||| |:| ||||| :|| | ||||| | :|||

Db 397 SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTTA 455

Qy 464 NIFPLLEDPTSENXTDEKKIEEKKAIQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT 523
 | ||||| |||| |||||:||||:| | ||||| | |||| | ||||| |:

Db 456 NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK 514

Qy 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583
 ||| |:||||||||||||||||| |||||||:||||| :||||| ||||

Db 515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574

Qy 584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP 642
 ||||:||||||||||||||||| :|||||:| | |||| |:|:| | ||||

Db 575 PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENP 634

Qy 643 PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSD 702
 |||||:|:| | | |||||: ||:||||||||||||||||| ||:||||:

Db 635 PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSSTEPSPDFSN 694

Qy 703 YSEMAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLKESLTETSFE 762
 |||:| |: |:|:|||||:|||||||||:| | |:| |||:|||| | |

Db 695 YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-E 753

Qy 763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822
 :: :: :|:| | | |||||: :| :| | :: |:| | | | | :

Db 754 TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT 811

Qy 823 AVYSNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHK 882
 |:| | | | | :|:|:||||||||||||| :|:| | | |:| | | |

Db 812 AIYSNDDLSSKEDKIKESETFSDDSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK 870

Qy 883 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS KVL LPPDVSA 942
 |||| | | ||| || | || | || | || :| :|:| | :| | :|:|

Db 871 SEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA 928

Qy 943 LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK 1002
 | | |: | | | | | | | | | | | | | | | | | | | | | | | |

Db 929 L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK 987

Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1062
 ||||| | | | | | | | | | | | | | | | | | | | | | | | |

Db 988 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFN 1122
 ||||| | | | | | | | | | | | | | | | | | | | | | | |

Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||||:|||||:|||||:|||||:
 Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 13

ABB81074

ID ABB81074 standard; protein; 1163 AA.

XX

AC ABB81074;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.

XX

PS Example 5; Page 44-47; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and

CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the rat
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 5; Length 1163;
 Best Local Similarity 74.0%; Pred. No. 6.2e-214;
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy	1	MEDLDQSPVLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK	58
Db	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK	60
Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP	118
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL	224
Db	167	RSGSGVDETLFALPAASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Qy	225	SPLSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS	284
Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDIFNEMQMSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396

XX
 AC AAY71557;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
 XX
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.
 XX
 OS Rattus sp.
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Example; Page; 122pp; English.
 XX
 CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
 CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were

CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC region was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 1162 AA;

Query Match 72.5%; Score 4294.5; DB 3; Length 1162;
Best Local Similarity 74.1%; Pred. No. 7.9e-214;
Matches 885; Conservative 103; Mismatches 156; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRQPAPFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
| | | : | | | | | | | | | | | | | | | | | | : | | : | | | | | | | | |
Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEDEDEEEEEDEEDEDLEELEVLERK 60

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSFVSSTVP 118
| | | | | | | | | | | | | | : | | : | | | | | | | | | | | | | : | | : |
Db 61 PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKR 178
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
| | | : | | | | | | | | | | | | | | | | | | : | | | | | | | | | | | |
Db 167 RGSGSVDETLEFALPAASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
| | | | | | | | | | | | : | | : | | : | | | | : | | : | | | | | | | |
Db 227 SPLSTVSFKEHGYLGNLSAVSSSEGTEETLNEASKELPERATNPFFVNRDLAEFSELEYS 286

Qy 285 EMGSSFSVSPKAESAVIVANPREETIIVKNKDEEEKLVSNNILHXQOELPTALTCLVKEDE 344
| | | | | | | | | | : | | : | | : | | : | | : | | : | | | | | | | | |
Db 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340

Qy 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403
| | | | | | | | | | : | | : | | | | | | | : | | | | | | | | | : | | |
Db 341 VVSPEKTMDFNEMQMSVAVPVREEYADFKPFEQAWVEVKDTEYEGSRDVLAA----RANVE 396

Qy 404 SKVDKKCFADSLEQTNHEKDSSESSNDDTSFSTPEGIKDRSGAYITCAPFNPAATESIAT 463
| | | : | | | | | | | | | | | | : | | | | | | | | | | | | | | | | |
Db 397 SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTTA 455

Qy 464 NIFPLLEDPTSENXTDEKKIEEKKQAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT 523
| | | | | | | | | | | | | | : | | | : | | | | | | | | | | | | | | | |
Db 456 NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK 514

Qy 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583
| | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574

Qy 584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP 642

Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSIGIKEEIKPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDFSDSIPDVPQKQDETVMVLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDFSDSIPDVPQKQDEAVMLMKESLTVS-E	753
Qy	763	SMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFIKSEAEQIRETETFSDDSSPIEIIDEFPTLISSKTDSESKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESETFSDDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSVA	942
Db	871	SEIANIQSGADSLPCLELPCDLSEFKNIYPK--DEVHVSDEFSENRRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFN	1107
Qy	1123	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKA	1177
Db	1108	GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA	1162

RESULT 15

AA71384

ID AAY71384 standard; protein; 1163 AA.

XX

AC AAY71384;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

```

XX
OS   Rattus sp.
XX
FH   Key          Location/Qualifiers
FT   Inhibitory-site 1. .171
FT                               /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                               /note= "Casein kinase II site"
FT   Region          31. .58
FT                               /note= "Acidic region"
FT   Region          172. .259
FT                               /note= "This region is not essential for inhibitory
FT                               activity"
FT   Misc-difference 223
FT                               /label= Unknown
FT                               /note= "There is Leu at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   233
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   242. .244
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   291
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   295
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 404
FT                               /note= "There is Ile at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   436
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   468. .470
FT                               /note= "Asn is N-glycosylated"
FT   Misc-difference 469
FT                               /label= Unknown
FT                               /note= "There is Lys at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   484
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   488
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   502
FT                               /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                               /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                               /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 661
FT                               /note= "There is Asn at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   694. .696
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   715
FT                               /note= "Casein kinase II site"
FT   Peptide         762. .1163

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FT /note= "used as immunogen to generate antibody AS Bruna"
 FT Modified-site 784
 FT /note= "Protein kinase C (PKC) site"
 FT Misc-difference 820
 FT /note= "There is Leu at this position in the sequence
 FT shown in AAY71310"
 FT Modified-site 821
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 850
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 855
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 863
 FT /note= "Casein kinase II site"
 FT Modified-site 868
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 893
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 912. .914
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 925. .927
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 954
 FT /note= "PKC and casein kinase II sites"
 FT Modified-site 956
 FT /note= "PKC and casein kinase II sites"
 FT Region 975. .1162
 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 976. .1163
 FT /note= "C-terminal common region found in Nogo A, B and C
 FT isoforms"
 FT Domain 988. .1023
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region"
 FT Modified-site 1024
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1071. .1073
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1073
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1089
 FT /note= "Protein kinase C (PKC) site"
 FT Domain 1090. .1125
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region"
 FT Modified-site 1141. .1143
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1143
 FT /note= "Protein kinase C (PKC) site"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 3; Fig 13; 122pp; English.

XX

CC The present sequence is an alternative version of rat Nogo A protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. Note: The present
CC sequence is an alternative version of the Nogo A sequence shown in Fig.
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC ID NO: 29 in disclosure of the specification. However the specification
CC does not include sequences for these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 72.4%; Score 4286.5; DB 3; Length 1163;
Best Local Similarity 74.1%; Pred. No. 2.1e-213;
Matches 886; Conservative 104; Mismatches 155; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
|||:|||| ||||| ||||| ||||| ||||| |||||:||||:|||||
Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEDDEEEDEEDEDLEELEVLERK 60

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVP 118
||||||| || ||| |||:|| :| ||||| ||||| |||||: || : |
Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPAPAPAAPSTPAAPKR 178
||| |||| ||||| ||||| ||||| || || ||||| |||||
Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
||| : ||||| |||||:||||| |||||

Db 167 RSGSGVDETLFALPAASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
 |||| |||| |||| | :||:| :|||: | :| :|| |||||

Db 227 SPLSTVSFKEHGYLGNLSAVSSSEGTIETLNEASKELPERATNPFVNRDLAEFSELEYS 286

Qy 285 EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDE 344
 ||||| || |||:| | :||:|:|:|:| : | : || || | ||

Db 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESVPG-----KEDR 340

Qy 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERWVEVKDSKEDS-DMLAAGGKIESNLE 403
 ||| || | || :|| | ||:|||||||: ||||: | | |:|| :|:|

Db 341 VVSPEKTMDFNEMQMSVVPVREEYADFKPFQAWEVKDTYEGSRDVLAA-----RANVE 396

Qy 404 SKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463
 ||||:| |||| : |||| |:| ||||| :|| | ||||| | :|||

Db 397 SKVDRKCLEDSELEQSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA 455

Qy 464 NIFPLLEDPTSENXTDEKKIEEKKAIIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLT 523
 | ||||| |||||:||||:| || ||||| || |||| ||||| |:|

Db 456 NTFPLLEDHTSENXTDEKKIEERKAIITEK-TSPKTSNPFVAVQDSEADYVTTDTLSK 514

Qy 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583
 ||| |:|||||:|||||:|||||:|||||:||||| ||||

Db 515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574

Qy 584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP 642
 ||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 575 PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP 634

Qy 643 PPYEEAMSVSLKVSGIKKEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD 702
 |||||:|:| | || ||||: ||:|||||:|||||:|||||:|||||

Db 635 PPYEEAMNVALKALGTKEGIKEPESFMAAVQETEAPYISIACDLIKETKLSTEPSDFSN 694

Qy 703 YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLESILTETSFE 762
 |||:| |: ||:|:|||||:|||||:|||||:| |:| ||:|||| | |

Db 695 YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVS-E 753

Qy 763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822
 :: :: :|:| | | |||||: :| :|| :|: ||:|||| |||| :|

Db 754 TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT 811

Qy 823 AVYSNDDLFIKSEAQIRETETFSDDSSPIEIDEFPFTLISSKTDSFSKLAREYTDLEVSHK 882
 |:|||| | | :|:|:|||||:|||||:| |:| || |:|||| |

Db 812 AIYSNDDLSSSKEDKIKESETFSDDSSPIEIDEFPFTFVSAKDDS-PKLAKEYTDLEVSDK 870

Qy 883 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVS 942
 |||| | |||| || || || || || :| :||:| |:| | :|:|

Db 871 SEIANIQSGADSLPCLLEPCDLSEFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA 928

Qy 943 LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK 1002
 | | |: |||| | | |||||: ||: |:| |||||

Db 929 L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK 987

Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1062
 |||||

Db 988 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1122
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 Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107
 Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
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 Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

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OM protein - protein search, using sw model

Run on: September 3, 2004, 16:02:30 ; Search time 23.2562 Seconds
(without alignments)
2615.013 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	931	15.7	199	2	US-08-700-607-1	Sequence 1, Appli
2	787.5	13.3	776	2	US-08-700-607-5	Sequence 5, Appli
3	705	11.9	356	2	US-08-700-607-6	Sequence 6, Appli
4	688	11.6	208	2	US-08-700-607-7	Sequence 7, Appli
5	671	11.3	267	2	US-08-700-607-8	Sequence 8, Appli
6	541.5	9.1	168	4	US-09-149-476-563	Sequence 563, App
7	513	8.7	241	2	US-08-700-607-3	Sequence 3, Appli
8	344.5	5.8	75	4	US-09-621-976-4600	Sequence 4600, Ap
9	344.5	5.8	75	4	US-09-621-976-4601	Sequence 4601, Ap
10	316	5.3	8991	4	US-08-714-741-32	Sequence 32, Appl
11	296.5	5.0	2468	4	US-09-976-594-726	Sequence 726, App

12	285	4.8	92	4	US-09-149-476-411	Sequence 411, App
13	276.5	4.7	1786	3	US-08-973-462-8	Sequence 8, Appli
14	267.5	4.5	1601	4	US-09-345-473E-40	Sequence 40, Appl
15	265	4.5	1596	4	US-08-978-277A-4	Sequence 4, Appli
16	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
17	256	4.3	1780	1	US-08-769-309A-5	Sequence 5, Appli
18	256	4.3	1780	3	US-08-994-570-5	Sequence 5, Appli
19	238	4.0	1346	2	US-08-635-121-2	Sequence 2, Appli
20	238	4.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
21	237.5	4.0	688	3	US-09-141-047-8	Sequence 8, Appli
22	237.5	4.0	1270	4	US-07-757-022B-44	Sequence 44, Appl
23	237.5	4.0	1311	4	US-07-757-022B-42	Sequence 42, Appl
24	237.5	4.0	1313	4	US-07-757-022B-142	Sequence 142, App
25	237.5	4.0	1314	4	US-07-757-022B-50	Sequence 50, Appl
26	237.5	4.0	1320	4	US-07-757-022B-46	Sequence 46, Appl
27	237.5	4.0	1320	4	US-07-757-022B-60	Sequence 60, Appl
28	237.5	4.0	1354	4	US-07-757-022B-48	Sequence 48, Appl
29	237.5	4.0	1361	4	US-07-757-022B-40	Sequence 40, Appl
30	237.5	4.0	1363	4	US-07-757-022B-52	Sequence 52, Appl
31	237.5	4.0	1404	4	US-07-757-022B-2	Sequence 2, Appli
32	237.5	4.0	1404	4	US-07-757-022B-62	Sequence 62, Appl
33	234.5	4.0	941	4	US-07-757-022B-14	Sequence 14, Appl
34	234.5	4.0	1022	4	US-07-757-022B-84	Sequence 84, Appl
35	234.5	4.0	1038	4	US-07-757-022B-74	Sequence 74, Appl
36	234.5	4.0	1049	4	US-07-757-022B-58	Sequence 58, Appl
37	234.5	4.0	1140	4	US-07-757-022B-104	Sequence 104, App
38	233.5	3.9	1320	4	US-10-164-595-58	Sequence 58, Appl
39	233.5	3.9	1404	4	US-10-164-595-78	Sequence 78, Appl
40	233.5	3.9	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
41	228	3.8	977	4	US-09-010-147B-18	Sequence 18, Appl
42	226.5	3.8	630	3	US-08-973-462-9	Sequence 9, Appli
43	225.5	3.8	2954	4	US-09-150-867-1	Sequence 1, Appli
44	225	3.8	783	6	5231168-2	Patent No. 5231168
45	225	3.8	3256	4	US-09-919-172-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304


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; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

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Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

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Qy      676 EAPYISIIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722
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Db      260 FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309

Qy      723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF 761
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; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

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Db      30 QYSILREEREAEELDSELI---IESCDASSASEESPKRE----QDSPPMK-----PSALDA 77

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Db      78 -----IREETGVRAEERAPSRRGLAEPGSFLDYPSTE-----PQPGPE----- 115

Qy      920 SDDFSKNGSATSKVLLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPTS 979
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Db      116 -----LPPGDGAL-----EPETPMLP-----RKPEEDSSSNQSPA 145

Qy      980 A-----IFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVS 1024
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Db      203 VVAYIALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFY 262

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Db      323 QAQIDQYLGLVVRTHINAVVAKIQAKIPGAKRHAE 356

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RESULT 4
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708

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Qy 1168 AKIPGLKRKAE 1178
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Db 198 AKIPGAKRHAE 208

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046
US-08-700-607-8

Query Match 11.3%; Score 671; DB 2; Length 267;
Best Local Similarity 66.3%; Pred. No. 1.1e-33;
Matches 124; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER APPLICATION NUMBER: 60/047,599
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; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER APPLICATION NUMBER: 60/047,593
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; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
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; EARLIER APPLICATION NUMBER: 60/047,501
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER APPLICATION NUMBER: 60/056,664
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; EARLIER APPLICATION NUMBER: 60/056,875
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; EARLIER APPLICATION NUMBER: 60/056,887
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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          9.1%; Score 541.5; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 5e-26;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

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Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178
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 Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607
 ; Patent No. 5858708
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,607
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 241 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: THP1NOB01
 ; CLONE: 31870

US-08-700-607-3

Query Match 8.7%; Score 513; DB 2; Length 241;
 Best Local Similarity 47.7%; Pred. No. 4.7e-24;
 Matches 102; Conservative 37; Mismatches 55; Indels 20; Gaps 1;

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Db 20 AEPSAPGGGGSPGACPALGTKSCSSSCAVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSV 79

Qy 1023 VSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSAL 1082
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Db 80 ISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139

Qy 1083 GHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYE 1142
 |:| :| : |||||:||||| || ||: |||||:||||| : : ||:|

Db 140 VHINRAKLIIRLFLVEDLVDLSKLAVFMWLMTYVGAVFNGITLLILAELLIXSVPIVYX 199

Qy 1143 RHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRK 1176
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Db 200 KY-----KVPSKTPWNRQK 213

RESULT 8

US-09-621-976-4600
 ; Sequence 4600, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 4600
 ; LENGTH: 75
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: 58
 ; OTHER INFORMATION: Xaa = His,Pro
 ; NAME/KEY: UNSURE
 ; LOCATION: 28
 ; OTHER INFORMATION: Xaa = Met,Val
 ; NAME/KEY: UNSURE
 ; LOCATION: 19
 ; OTHER INFORMATION: Xaa = Pro,Gln
 ; NAME/KEY: UNSURE
 ; LOCATION: 53
 ; OTHER INFORMATION: Xaa = Ser,Tyr
 US-09-621-976-4600

Query Match 5.8%; Score 344.5; DB 4; Length 75;
 Best Local Similarity 82.6%; Pred. No. 1.9e-14;
 Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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Db 1 MEDLDQSPLVSSSDSPPRXQPAFKYQFXREPEDEE-----EDLEELEVLERKPA 49

Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86

Db ||| |||| | |||||||||
50 AGLXAAPVXTAPAAGAPLMDFGNDEFV 75

RESULT 9

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US-09-621-976-4601
; Sequence 4601, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4601
;   LENGTH: 75
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 58
;   OTHER INFORMATION: Xaa = His,Pro
;   NAME/KEY: UNSURE
;   LOCATION: 28
;   OTHER INFORMATION: Xaa = Met,Val
;   NAME/KEY: UNSURE
;   LOCATION: 19
;   OTHER INFORMATION: Xaa = Pro,Gln
;   NAME/KEY: UNSURE
;   LOCATION: 53
;   OTHER INFORMATION: Xaa = Ser,Tyr
US-09-621-976-4601

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Query Match 5.8%; Score 344.5; DB 4; Length 75;
Best Local Similarity 82.6%; Pred. No. 1.9e-14;
Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

[illegible]

RESULT 10

US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.

```

; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

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Query Match          5.3%; Score 316; DB 4; Length 8991;
Best Local Similarity 21.4%; Pred. No. 9.9e-10;
Matches 248; Conservative 138; Mismatches 479; Indels 296; Gaps 52;

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Qy      6 QSPLVSSSDSP-PRPQPAFKYQF-VREPEDEEEEEEEEEDEDEDLEE--LEVLERKPAA 61
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Db      7193 EAPAEQPKPAPAPQAPAPKPEKPAPAEQPKPEKTDDQQAEDYARRSEEEYNRLTQQQPPK 7252

Qy      62 GLSAAPVP-----TAPAAG-----APLMDF 81
      || |      | | |      | |
Db      7253 AEKPAPAPKTGWKQENGWYFYNTDGSMGEQAGQYRAAAEGDLAAQAELEKTEADLKKA 7312

Qy      82 GNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPED---DE 138
      |: |||      || | || || |:|      ||| |      | : : | :|
Db      7313 VNEPEKPAPAPETPA--PEAPAEQPK--PAPAPQAPAPKPEKPAPAEQPKAEKTDDQQAEE 7368

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Qy 139 PPAR-----PPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXX 189
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 Db 7369 DYARRSEEEYNRLTQQQPPKAEKPAPAPKPEQPAPAPKNSKGEQAEQYRSAAGGDLAAKQ 7428
 Qy 190 XKI----MDLKEQPGNTISAGQEDFPSVLLET-AASXPSSLSPLSAASFKEHEYLGNLSTV 244
 : : ||| : : : | : | : :
 Db 7429 VELEKTEADLKK-----AVNEPEKPAPAPETPAPEAPAEQPKPAPAPQ----- 7471
 Qy 245 LPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVAN 304
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 Db 7472 -PAPAPKPEKPAEQPK--AEKPADQQAEDYDRRSEEEYNRL--TQQQPPKAEKPAPAPQ 7526
 Qy 305 PREEI-----IVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNE 357
 | : : | : : | || || | : : | : |
 Db 7527 PEQPAPAPKSLKEIDESSEDYVKEGFRAPLQSELDQAKLSKLEEL-----SDKIDE 7580
 Qy 358 KRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQ 417
 : | : : || || || : : | : || ||||
 Db 7581 LDAEI-AKLEKDVEDFK-----XSDGEQAGQYLAAAEEDLIAKKA---ELEQ 7623
 Qy 418 TNHEKDSSESSNDDTSFPS---TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTS 474
 | | : : : | : || || || |
 Db 7624 T--EADLKKAVNEPGKPAPAPAPE-----TPAPEAPAEQPK-----PAP 7660
 Qy 475 ENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYV--TTDNLTKVTEEVVA-- 530
 | | : | || | : || : : : : |
 Db 7661 ETPAPAPKPEKPAEQPKPEK-----PADQQAEDYARRSEEEYNRLTQQQPAPA 7709
 Qy 531 -----NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584
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 Db 7710 QKPEQPAKPEKPAEEPTQPEKDAEIAKLE-KNVEYFKKTDAEQTEQYLAAAEKDLADKKA 7768
 Qy 585 SFESEA-----TPSPV-LPDIVMEAPLNSAVPSAGASVIQPSSSPLEAS 628
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 Db 7769 ELEKTEADLKKAVNEPEKPAAETPAPAPKPEQPAEQPKPAPAPQP-APAPKPEKTDDQQA 7827
 Qy 629 SVNYESIKHEPENPPPYEEAMSVSLKVSGIKEE---IKEPENINAALQETEAPYISIIAC 684
 : | | | : : | | : || | : |
 Db 7828 EEDYARRSEEEYNRLPQQQPPKAEKPAPAPKPEQPVPAEXPEN-----PAPAPKPAXAP 7881
 Qy 685 DLIKETKLSAEPAPDFSDYSEMAKVEQPV-----PDHSELVEDSS-----PDS 727
 : | : : : | : | : | : |
 Db 7882 QPLKPEEPAEQPKPE-----KPEEPAGQPEPEKPDQQAEDYARRSGGEYNRFPQQ 7933
 Qy 728 EPVDLFSDDSIIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGG----- 781
 : | | : : | | | | || :
 Db 7934 QPPKAEKPAPAP----KPEQVPAPKTL-----KKAKLAGAKSKAATKKAEL 7977
 Qy 782 KPYLESFKLSLDNTKDTLLP-----DEV-----STLSKK-EKIPLQMEELSTAVYSNDD 829
 : | || : | : || | : : | : || | : | : : |
 Db 7978 EPELEKAEAELENLLSTLDPEGKTQDELDKEAAEALNKKVEALPNQVSELEEEELSKLED 8037
 Qy 830 LFISKEAQIRETETFSDSPIEIIDEFPTLISSKTDSFSKLARE----YTDLEVSHKSEI 885
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 Db 8038 NL--KDAETNNVEDY-----IKEGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 8088

Qy 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259
 : | | | : : : | : | : | : | : : | : :
 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFSRSA 1222

 Qy 260 -----KEVSEKAKTLLIDRDLTEF-----SELEYSEMGS---SFS 291
 | | | | : | | | : | : | : | :
 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPPSKSPSLSPSPSPLEKTPLGERSNVFS 1280

 Qy 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328
 : : | | : | : : : : | : : | : : |
 Db 1281 LTPNEIKVSAEAEVAPVSPEVTQEVVEHCASPEDKTLEVVSQS SVTGSAGHTPPYQSP 1340

 Qy 329 ----QQELPTALTCLVKEDEVSSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383
 | | : : | | : | : : | : | | : | : |
 Db 1341 TDEKSSHLPTEV--IEKPPAVPVSFEFSDAKDENERASVSPMDPEVPDSESPIEKVLSPL 1398

 Qy 384 DSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDR 443
 | : : | | : | | | : : | | :
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEESKSGKQGS PDQVSPVSE----- 1447

 Qy 444 SGAYITCAPFNPAATESIATNIFP LLEDPTS ENXTDEKK-----IEKK-----A 488
 : | | : | : | | | : : : : : :
 Db 1448 ----MTSTSLYQDKQEGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLG DVSP 1503

 Qy 489 QI-----VTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVA--N 531
 | : | | : | | : | | : : | : | :
 Db 1504 QIDVSQFGSKEDTKMSISEGTVSDKSATP--VDEGVAEDTYSHMEGVASVSTASVATSS 1561

 Qy 532 MPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES-LYPAAQLCP----- 584
 | | | : : : | : : : : | | : : | : |
 Db 1562 FPEPTTDD-VSPSLHAEVGS PHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRMSIS 1620

 Qy 585 -----SFESEATPSPVLP-DIVMEAPLNSAVPSAGASVI 618
 | | : : | | : : | : | : | :
 Db 1621 PPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPDH---PTVGAGVL 1677

 Qy 619 Q-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSGIKEEIKE 664
 | : | : | : | | | : | | : : |
 Db 1678 HITENGPTVDYSPSDMQDSSLSHKIPMEEPSYTQDNDLSELISVSQVEASPSTSSAHT 1737

 Qy 665 PENINAALQETE----AP-----YISIACDLIKE---TKLSAEP-----A 697
 | | : | | | | : : : | | : :
 Db 1738 PSQIASPLQEDTLSDVAPPRDMSLYASLTSEKVSLEGEKLSPKSDISPLTPRESSPLY 1797

 Qy 698 PDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFS----- 734
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 Db 1798 PTFSDSTSAVK-EKTATCHS----SSSP---PIDAASAEPYGFRA SVLFDTMQHHLALNR 1849

 Qy 735 DDSIPDVP-----QKQDETVM LVKESLTETSFESMIEYENKEKLSALPPE 779
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 Db 1850 DLSTPGLEKDSGGKTPGDFSYAYQKPEET-----TRSPDEEDYDYESYEKTTRTSDV 1901

 Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDL FISKEAQIR 839
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 Db 1902 GGY-YYEKIERTTKSPSDSGYSYE--TIGKTTKTP-----EDGDYSYE--IIEKTTTRTP 1950

QY 840 ETETFSDDSSPIEIIDFPTLISSKTDSD---FSKLAREYTDLEVSHKSEIANAPDGAGSLP 896
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 Db 1951 EEGGYSYD-----ISEKTTSPPEVSGYSYEKTERSRRLLDDISNGYDDS---- 1994

QY 897 CTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSXVLLLPDVSALGHTQAE-IESIVK 955
 : | | : : ||| : : || | : || | :
 Db 1995 -EDGGHTLGDPSSYSYETTEKITSFPESEGYSETSTKTTRTPDTSTYCYETAEKITRTPQ 2053

QY 956 PKVLEKE-----AEKKLPSDTEKE 974
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 Db 2054 ASTYSYETSDLCYTAEKKSPSEARQD 2079

RESULT 12

US-09-149-476-411

; Sequence 411, Application US/09149476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: PZ002P1
 ; CURRENT APPLICATION NUMBER: US/09/149,476
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/038,621
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,626
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 ; EARLIER APPLICATION NUMBER: 60/047,600
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,615
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,597
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,502
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
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; EARLIER APPLICATION NUMBER: 60/047,584
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; EARLIER APPLICATION NUMBER: 60/047,492
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; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,674
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER APPLICATION NUMBER: 60/056,662
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; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,637
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; EARLIER APPLICATION NUMBER: 60/056,903
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; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,636
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; EARLIER APPLICATION NUMBER: 60/056,845
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; EARLIER APPLICATION NUMBER: 60/057,761
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
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; EARLIER APPLICATION NUMBER: 60/047,588
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; EARLIER APPLICATION NUMBER: 60/047,586
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23


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; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
```

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Query Match          4.8%;  Score 285;  DB 4;  Length 92;
Best Local Similarity 57.1%;  Pred. No. 1.2e-10;
Matches 52;  Conservative 20;  Mismatches 19;  Indels 0;  Gaps 0;
```

```
QY      1079 NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTLLILALISLFSVP 1138
          |:|: |:|  :| : |||||:||||| || ||: |||||:||||:||||| : :|||
Db      2  NAAMVHINRAKLIIIRLFLVEDLVDLSKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61

QY      1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1169
          ::||::: |||||:|:|  | : || :|
Db      62  IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92
```

RESULT 13
 US-08-973-462-8
 ; Sequence 8, Application US/08973462B
 ; Patent No. 6191270
 ; GENERAL INFORMATION:
 ; APPLICANT: DRUILHE, PIERRE
 ; APPLICANT: DAUBERSIES, PIERRE
 ; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
 ; FILE REFERENCE: 0660-0125-0 PCT
 ; CURRENT APPLICATION NUMBER: US/08/973,462B
 ; CURRENT FILING DATE: 1998-02-06
 ; EARLIER APPLICATION NUMBER: PCT/FR96/00894
 ; EARLIER FILING DATE: 1996-06-12
 ; EARLIER APPLICATION NUMBER: FR 95/07007
 ; EARLIER FILING DATE: 1995-06-13
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 1786
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
 US-08-973-462-8

Query Match 4.7%; Score 276.5; DB 3; Length 1786;
 Best Local Similarity 20.1%; Pred. No. 2.6e-08;
 Matches 232; Conservative 201; Mismatches 471; Indels 249; Gaps 50;

Qy	30	EPEDEEEEEEEEDEDEDLEE-----LEVLERKPAAGLSAAPVPTAPAAGAPLMDFGN	83
		: : : : : : : : : ::	
Db	228	EESVEENDEESVEENVEENVEENDDDGSSVASSVEESIASSVDESIDSSIEENVAPTVE---	284
Qy	84	DFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAPSPLSAAAVSPSKLPEDDEPPAR-	142
		: : : : : :	
Db	285	EIVAPS-----VVESVAPSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAEN	338
Qy	143	-----PPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQ	198
		: : : : ::	
Db	339	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	398
Qy	199	PGNTISAGQEDFPSVLLETAAS-----XPSLSPLSAAASFKEHEYLGNLSTVLPT-EGTL	251
		: : : : :: : : : : : : ::	
Db	399	VAENV---EESVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESV	455
Qy	252	QENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVI-----VANP	305
		: : : : : : : : :	
Db	456	EENVEESVAENVEESVAENVEESVAENVEESVAE-NVEESVAENVEESVAENVEESVAEN	514
Qy	306	REEIIVKNKDE-----EEKLVSNNILHX-----QQELPTALTKLVKED-----EVV	346
		: : :: : :: : : : : : :	
Db	515	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	574
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYA-----DFKPFERVWEVKDSKEDSDMLAAGGKIESN	401
		: :: : : : :	
Db	575	VAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEES-----VEEN	626


```
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1601
; TYPE: PRT
; ORGANISM: C. elegans
US-09-345-473E-40
```

```
Query Match          4.5%; Score 267.5; DB 4; Length 1601;
Best Local Similarity 20.5%; Pred. No. 8e-08;
Matches 229; Conservative 134; Mismatches 376; Indels 377; Gaps 56;
```

```
Qy      29 REPEDEEEEEEEEE-----EDEDLEDLEEVLERKPAAGLSAAPVPTAPAAGA 76
      | :|| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      462 RAKEEEERIREAEIKEELRLRAEAKEKEKERLEK-ERLEKKAAAAAANPNPTP----- 515

Qy      77 PLMDFGNDFVPPAPRGP-----LPAAPPVAPE-----RQPSWDPS-PVS--STVPAPSP 122
      :|| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      516 -----IPPTPATPHSSAQQQPIPPPLSTQTSAEIQQSAQQPSVPVTMIANIPAMSP 566

Qy     123 LSA---AAVSPSK----LPEDDEPPARPPPPPPASVSPQAEPVW---TPPAPAP--AAPP 170
      || :||: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     567 TSAQPQFVLSPTSAAVPVPTTMIHVPKPSEIPVQNVATTAAPVAANNVPPSPAPFKTEDI 626

Qy     171 STPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAG-QEDFPSVLLETAASXPSLSPLSA 229
      || : | | | | | | | | | | | | | | | | | | | | | | | |
Db     627 QTPTLAQ-----NTVPTISTDASGLVINTPASIASPSPAPS 663

Qy     230 ASFKEHEYLGNLSTVLP-----TEG-----TLQENVSEASKEVSEKAKTLLIDRDLT 276
      |: : : | | | | | | | | | | | | | | | | | | | | | |
Db     664 AT----DVA STTAPVTPAPTPTTTTDGGAAAASTTTENKEEKRKSNKRKVVM EILGCDES 719

Qy     277 E-----FSELEYSEMGSFSVSP-----KAESAVIVANPREEIIVK 312
      |: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     720 RNFALVSCRLDTSHKSVTFQFAPGTDKPCTIATKLLAEDCLLKVVHIVEAQLGEVIQLI 779

Qy     313 NKDEEE----KLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMRE 368
      | | :: | | : :| | :| :: :| | | | : :: :
Db     780 NSDGKKGVGTKLAT--VLDPNSTEPPTITAVMPKD----SSAATASNTKPKIEI----- 827

Qy     369 EYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESN 428
      |: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     828 -----EKTPTTRDASQE-----PNNVQVTNVRKVSQESN 856

Qy     429 DDTSF PSTPEGIKDRSGAYITCAPFN-----PAAT---ES 460
      : | | | | | | | :| | | | | | | | | | | | | | | |
Db     857 AE-SVQSIP-----RPGGIIVMSPTNQTD SAPPTGAAAKPSRFQVTKSADPIATPISSS 910

Qy     461 IAT-NIFPLLEDPTS ENXTDEKKIEEK-KAQIVTEKNTSTKTSNPFVAAQDSE TDYVTT 518
      |:| :| :: | | | | | :| | ::| | :| :| :| :| :| |
```

Db 911 ISTATVIPIVA-ATPTNITSEPVIVQPITAQVITHLATPSPVSHSL---SSNSSPSATTH 966
 Qy 519 DNLTKVTEEVVANMP-EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLY 577
 |::: : :| | :| | :| |
 Db 967 SNMSSI--QSTTSVPGRFTVQPVSA-ESGISSSISTPHPEPT----- 1007
 Qy 578 PAAQLCPSFEESEATPSPVLPDIMEAPLNSAV-----PSAGASVIQSSSPLEASSVNY 632
 || || | :| :| || | || : | ||:
 Db 1008 PAITSCP-----PPVPSVPPVVSNGTLNLEVAPKQTPSATNQNVDTQHSSSTASTATL 1060
 Qy 633 ESIKHEPEN-----PPPYEEAMSVS-----LKVSGIKEEIKEPENINAA 671
 : | | :| : : |||: | : :
 Db 1061 --VSETPATVHVTPISVPAPVQEPLVIDHSDVLTQLDSELRKVSGVSHS-ASPSTVVES 1117
 Qy 672 LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVD 731
 | :|| : : || : :
 Db 1118 LTSMTPTIPLACQTV-PASIGQAPAVIAAHA-----AS 1151
 Qy 732 LFSDDSIIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS 791
 | :|:| | :| || : ||| || |:
 Db 1152 LIPNASVPQSPSRLD-----AETGLAGL-----HEKLEAL-----KME 1184
 Qy 792 LDNTKDTLLPDE---VSTLSKKEKIPLQ-----MEELSTAVYSNDDLFISKEAQIRET-- 841
 | :| :|: :| | :||: || :||
 Db 1185 QDRRED--MGDDAIGTTTTDGKDEIPIDTLKGLAEALGKVIHADG-----RETTP 1232
 Qy 842 -----ETFSDDSPIEII-----DEFPTLISSKTD SFSKLAREYTDLEVS--HKSEIANAP 889
 :|:| :| | :| :| | | | : :|
 Db 1233 MPPDHPDLTDASTQQLISPSNPDLTTMSSAVEGSASSTMIEDIDASTSAVDASMMNSMP 1292
 Qy 890 DGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLLPPDVSA LGHTQAE 949
 || :| : :| | | | : : | |
 Db 1293 PGA-----QNSTDQIPAAMTSLMDQECAQSMTSSITR-----NTTGTKLAT 1333
 Qy 950 IESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAD 985
 |:: | | | | :| | |
 Db 1334 FENL-----ETALSSTLGTHIRQPNAPSSRD 1359

RESULT 15

US-08-978-277A-4

; Sequence 4, Application US/08978277A

; Patent No. 6582956

; GENERAL INFORMATION:

; APPLICANT: Gelman, Irwin H.

; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10112-0228

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/978,277A
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/665,401
;   FILING DATE:  18-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Clark, Richard S
;   REGISTRATION NUMBER:  26,154
;   REFERENCE/DOCKET NUMBER:  A30558 - 165/34008
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  212-408-2558
;   TELEFAX:  212-765-2519
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1596 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FRAGMENT TYPE:  internal
;   ORIGINAL SOURCE:
US-08-978-277A-4

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Query Match          4.5%;  Score 265;  DB 4;  Length 1596;
Best Local Similarity 21.3%;  Pred. No. 1.1e-07;
Matches 232;  Conservative 145;  Mismatches 422;  Indels 288;  Gaps 47;

```

```

Qy      2 EDLD--QSPLVSSSDSPPRPQPAFKYQFVREPEDE-----EEEEEEEEDEDEDLEELEV 54
      |:|:  :|  :||:|  |  |  :|  ||::  ||  :  :  |
Db      620 EELEKVKSATLSSTDST-----VSEMQDEVKTVGEEQKPEEPKRRVDTSVSWEA 668

Qy      55 LERKPAAGLSAAPVPTAPAAGAPL-----MDFGNDVFPPAPR----- 91
      |  ::  |  ::  |  |  :  |  ||  :  :
Db      669 LICVGSSKKRARKASSSDDEGGPRTLGGDSHRAEEASKDKEAGTDAVPASTQEQQDAQGS 728

Qy      92 -GPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPAS 150
      |  ||  |  |  :  :  |  :  |  ||  |  |  :
Db      729 SSPEPAGSPSEGEVSTWE-----SFKRLVTPRKK---SKSKLEEKAEEDSS--VEQLSTE 778

Qy      151 VSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAG---- 206
      :  |  |  |  :  |  |  :  |  |  :  :  |
Db      779 IEPSREESWV-----SIKKFIPGRRKKRA-----DGKQEQTATVEDSGPVEI 819

Qy      207 QEDFPSVLLETAASXPSLSPLSAAAFKEHEYL---GN-----LSTVLPTEGTLQENVSE 257
      ||  |:|  |  :  ||  :  |  |  :  |  |  :  |
Db      820 NEDDPNV-----PAVVPLSEYNAVEREKMEAQGNTELPQLLGAVYVSE-----E 863

Qy      258 ASKEVSEKAKTLLID--RDLTEFSELEYSEMGSSFVSVPKAESAVIVANPREEIIIVKNKD 315
      ||  :  :  ||  |  :  |  |  :  :  |  :  |  ||  :  :
Db      864 LSKTLVHTVSVVAVIDGTRAVTSVEERSPSWISASVT-EPLEHTAGEAMPVVEEVTEKDII 922

```

Qy 316 EEEKLVSNILHXQQELPTALTCLVKE-----DEVVSSEKAKDSFNEKRVAVEAPMREEY 370
 || | ||: | ||: || | || |
 Db 923 AEETPV-----LTQTLPEGKDAHDDMTSEVDFTS-----EAVTATET 960

Qy 371 ADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKCFADSLEQTNHEKDSSESNDD 430
 :: | | | :: | | | :: : | : | : | |
 Db 961 SEALRTEEVTEASGAETTDMVSAVSQLTDS-----PDTTEEATPVQEVESGVL 1010

Qy 431 TS-----FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEK 481
 | : : | | : : | | : : | :
 Db 1011 TEEERQTQAILQAVADKVKEES-----QVPATQTVQRTGSKALE-----KVE 1053

Qy 482 KIEEKKAIQVTEKNTSTKTSNPFVFA-----AQDSETDYVTTDNLTKVTEEVVANMPEGL 536
 : || : || | | || | | || |
 Db 1054 EVEEDSEVLASEKEKDVMPKGPVQEAGAHLAQGSETQAT-----PESL 1098

Qy 537 TPDVLQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFEESEATPSPV 596
 | : || : : : : : | : : || |
 Db 1099 -----EVPEVT-ADVDHVATCQVIKLQQLMEQAVAPES--ETLTDSETNGSTP 1144

Qy 597 LPD-----IVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMS 650
 | | : : | | : | : | : | | |
 Db 1145 LADSDTADGTQQDETIDSQDSKATAAVRQSQVTEEEAATAQKEEPSTLPNNVPAQE---- 1200

Qy 651 VSLKVSIGIKEEIKPENINAAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVE 710
 | : || | : | : : : | | : | | |
 Db 1201 -----EHGEEPG--RDVLEPTQQELTAAAVPVLAKTEVGQEGEVDWLD-GEKVKEE 1248

Qy 711 QPVPDHSSELVEDSSPDSE-PVDLFSDDSIQDVPQKQD-ETVMLVKESLTETSFESMIEYE 768
 | | | | : | : | : | : | : | | : | |
 Db 1249 QEVFVH-----SGPNSQKAADVTDSEVMGVAGCQEKESTEVQSLSLGEGEMETDVEKE 1302

Qy 769 NKE-KLSALPPEG-----GKPYLESFKLSLDNTK-----DTLLPDEVSTL 807
 : | | : || || | | : | ||:
 Db 1303 KRETKPEQVSEEGEQETAAPHEGTYGKPVLTLDMPSSSERGKALGSLGGSPSLPDQ---- 1358

Qy 808 SKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDS--SPIEIDE--FPTLISSK 863
 | | : : | | : : || | : | | | |
 Db 1359 DKAGCIEVQVQSLDTTVTQTAEAV----EKVIETVVISETGESF-ECVGAHLLPAEKSSA 1413

Qy 864 TDSFSLKAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLKNIQPKVVEEKISFS--- 920
 | | : : : | : | | : | : : | |
 Db 1414 TGGHWTLQHAEDTVPLGPESQ-----AESIPIIVTPAPES--TLHPDLQGEISASQRE 1464

Qy 921 -----DDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLP 968
 | | : | || | : | : | : | :
 Db 1465 RSEEDKPDAGPDADGKESTAIEKVLKAEPEILELESKSNKIVLNVITQAVDQFARTETA 1524

Qy 969 SDTEKED 975
 : | |
 Db 1525 PETHAYD 1531

Search completed: September 3, 2004, 16:10:38
 Job time : 27.2562 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:00:14 ; Search time 25.1547 Seconds
(without alignments)
4504.667 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	787.5	13.3	776	2	A46583	neuroendocrine-spe
2	688	11.6	208	2	I60904	neuroendocrine-spe
3	671	11.3	267	2	A60021	tropomyosin-relate
4	528	8.9	2484	2	T26216	hypothetical prote
5	519.5	8.8	2607	2	T26215	hypothetical prote
6	340.5	5.7	222	2	T26213	hypothetical prote
7	331	5.6	7962	2	I38346	elastic titin - hu
8	325.5	5.5	5327	2	T13564	microtubule-associ
9	324.5	5.5	865	2	A47282	calcium-binding pr
10	320.5	5.4	873	2	A47283	calphotin - fruit
11	299.5	5.1	3488	2	T34418	hypothetical prote
12	299	5.0	3924	2	S37431	ankyrin 2, neurona
13	290.5	4.9	1274	2	T16251	hypothetical prote

14	289	4.9	2364	2	A56577	microtubule-associ
15	289	4.9	2464	1	QRMSP1	microtubule-associ
16	287.5	4.9	971	2	T19431	hypothetical prote
17	285.5	4.8	1621	2	A82255	hypothetical prote
18	278	4.7	1948	2	S00485	gene 11-1 protein
19	274	4.6	3507	2	T34513	hypothetical prote
20	272.5	4.6	1829	2	T24583	hypothetical prote
21	272.5	4.6	2361	2	T25752	hypothetical prote
22	271	4.6	2187	2	T30826	nascent polypeptid
23	270	4.6	1230	2	T22458	hypothetical prote
24	267.5	4.5	1851	2	T19964	hypothetical prote
25	263.5	4.4	2409	1	A60979	versican precursor
26	262.5	4.4	6642	2	T29757	protein UNC-89 - C
27	261	4.4	1558	2	B71603	RESA-H3 antigen PF
28	260.5	4.4	3381	2	T42389	versican precursor
29	259.5	4.4	1828	2	A40115	microtubule-associ
30	258	4.4	1616	2	G64242	cytadherence-acces
31	257.5	4.3	5170	2	T15348	hypothetical prote
32	256	4.3	990	2	I51618	nucleolar phosphop
33	256	4.3	1634	2	T26517	hypothetical prote
34	255.5	4.3	1684	2	JW0057	gravin - human
35	253	4.3	1189	2	S56852	hypothetical prote
36	252.5	4.3	1224	2	T14007	microtubule-associ
37	252	4.3	4377	2	A55575	ankyrin 3, long sp
38	250.5	4.2	1824	1	QRHUMT	microtubule-associ
39	250.5	4.2	1830	2	A37981	microtubule-associ
40	248	4.2	1825	2	S13507	microtubule-associ
41	248	4.2	1890	2	T04556	hypothetical prote
42	248	4.2	3421	1	WZBEB6	367K tegument prot
43	246	4.2	1110	2	I51116	NF-180 - sea lampr
44	244.5	4.1	1029	2	T30351	mucin-like protein
45	243	4.1	1320	2	JC5630	TCOF1 protein - mo

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 13.3%; Score 787.5; DB 2; Length 776;
Best Local Similarity 31.9%; Pred. No. 3.1e-25;
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

Qy	588	ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY----	632
		: : : : : : :	
Db	141	EELGTPGPSLDPDVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDIT	200
Qy	633	--ESIKHEPENPPPYEEA-----MSVSLKVSIGIKEEIKEPENINAAL-----QET	675
		: : :: : : : : :	
Db	201	RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST	259
Qy	676	EAPYISIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED	722
		: : : : : : :	
Db	260	FAPYID---DLSEEQRRAPOITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK	309
Qy	723	SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF	761
		: : : : :	
Db	310	PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQKGKSISEDELITAIKEA-----	363
Qy	762	ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS	821
		: : : : :	
Db	364	-KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA	403
Qy	822	TAVYSNDDLFISKEAQIRETETFSDSPIEIDEFP----TLISSKTDSEFS-----	868
		:: : :	
Db	404	SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP	444
Qy	869	-----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDSLKNIQPKVEEKISFSD	921
		: : : : :	
Db	445	ASPSIQYSILREERAELDELIIESCDASSAS-----EESPKREQDSPMPKPSALD	496
Qy	922	DF-----SKNGSATSKVLL-----LPPDVSA LGHTQAEIESIVKP	956
		: : :	
Db	497	AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQGPPELPPGDGAL-----EPETPMLP	551
Qy	957	KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK	1001
		: : : : : :	
Db	552	-----RKPEEDSSSNQSPAATKGPGPLGPGAPPPLLF---LNKQKAIDL YWRDIK	599
Qy	1002	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRA	1061
		: : : : : : : :	
Db	600	QTGIVFGSFLLLFLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKA	659
Qy	1062	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1121
		: : : : : : :	
Db	660	YLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALF	719

QY 1122 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
| | | | :
Db 720 NGLTLLMAVVSMTFLPVVVKHQEQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 776

RESULT 2

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R; Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 11.6%; Score 688; DB 2; Length 208;
Best Local Similarity 67.5%; Pred. No. 6.2e-22;
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

QY 988 KTSVVDDLlyWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1047
 |: :|||||||::||:|: | || ||| |:||| |:||| || ||||| | :
Db 18 KSOAIDLlyWRDIKOTGIVFGSFLLLLFSLTQFSVVSVVAYIALAALSATISFRIYKSVL 77

Qy 1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
 ||:||:|||||:|||| |: :||: |::| :|||: :|| |:||||| |||||
Db 78 QAVOKTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKF 137

QY 1108 AVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
 ||||: |||||:|||||:||||:||||:||||:||||:||||: |||| :: :|||
 Db 138 AVLMWLLTYVVGALFNGLTLLLMVVSMTFLPVVYVKHQAQIDQYLGIVRTHINAVVAKIQ 197

Qy 1168 AKIPGLKRKAE 1178
||| || ||
Db 198 AKIPGAKRHAE 208

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C>Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text_change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 11.3%; Score 671; DB 2; Length 267;
Best Local Similarity 66.3%; Pred. No. 4.4e-21;
Matches 124; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

```
Qy      988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1047
          |: :|||||||:|:|:|: | || ||| |:| | |:| | | ||||| |:
Db      9   KSQAIDLLYWRDIKQTGIVFGSFLLLFLSLTQFSVSVVAYLALAALSATISFRIYKSVL 68

Qy     1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
          ||:|:|:|||||:| | | |: :|:| :| | :| | | | | | | | | | | |
Db      69   QAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDLSLKF 128

Qy     1108 AVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
          |||||: ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db      129 AVLMWLLTYVGALFNGLTLLLLMAVSMFTLPVVVYVKHQAQVDQYLGVLVRTHINTVVAKIQ 188

Qy     1168 AKIPGLK 1174
          ||||| :
Db      189 AKIPGAR 195
```

RESULT 4

T26216

hypothetical protein W06A7.3c - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 8.9%; Score 528; DB 2; Length 2484;
Best Local Similarity 20.9%; Pred. No. 7.4e-14;
Matches 277; Conservative 186; Mismatches 461; Indels 402; Gaps 54;

```
Qy      1   MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEE-----EE 38
          :| :: |   | :| |   | |:| | :|
Db     1397 LEKVEVQP--DLSQNSPAPHKIIDLHF-NIPKDHEDYGNDYVPFGTESSEESQKADGNQE 1453
```

Qy	39	EEEEED-----EDEDLEELEVLERKPA-----AGLSAAP-----	67
		: : : :	
Db	1454	NQEEDDVVAELNFHPIRQWRDEDEVISLQSLKSLVAEVGCITDVDASDVNEQDEESTLKIL	1513
Qy	68	--VPTAPAAGAPIMDFGNDFVPAPRGPLPAAPPVAP--ERQPSW-----	108
		: : : : :	
Db	1514	KVVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV	1569
Qy	109	-----DPSPVSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW	159
		: : :	
Db	1570	TESEISEMAPQVSESTCPIPEPL-----ADLKLPVEDDEKTPEPEPVVPGVQVERIIPIE	1624
Qy	160	TPPAPA-PAAPPSTPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQEDFPSVL--LE	216
		: : :	
Db	1625	VEQAPTIPQRPPRAP-----KSELPKVAKPLD	1651
Qy	217	TAASXPSSLPLSA-----ASFKEHEYLGNLSTVLPTEGLQENVSEASKEVSEKAKTLL	270
		: : : : : : : : : : :	
Db	1652	DSKSRVRFAPLNKLGRTYSEEQQKELVESLERPL-TIITQQKPPEKPTEDIG--ALSPL	1708
Qy	271	IDRDLTFESELEYSEMGSFSVSPAESAVIVANPREEIIVKNKDDEEEKLVSNNILHXQQ	330
		: : : : : :	
Db	1709	SPNTLAEEYEEVPMMDMQS-----VPHSPQE-----KQEEIEALSEII-----	1745
Qy	331	ELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAPMREEYADF---PFERVWEVKDSKE	387
		: : : : : : : : : :	
Db	1746	EEOAMKEVEKPE-SAPEKDNESELAPEI-INAPIRRVLVETKIMGPGKSLNEDNDDDD	1803
Qy	388	D-SDMLAAGGKIESNLISKVDKKCFADSLEQTNEHKDSESS----NDDTSFPSTPEGIKD	442
		: : : : : : : : : :	
Db	1804	DGSECLDSIGDLS---ERTIQR--FNIDSIDPSIRDRSFSSISSFGDRQKFRTAIENIRQ	1858
Qy	443	RSGAYITCAPFNPAATESIATNI FPLEDPTS ENXTDEKKIEEKKAQIVTEKNTSTKTSN	502
		: : : : : :	
Db	1859	-----DLLPFQSSVSQYLRSSNP-----SQQLLVTN-----	1885
Qy	503	PFFVAAQDSETDYVTTDNLTKVTEEVANMPGLT PDLVQEACESELNEVTGTKIAYETK	562
		: : : : : : : : : :	
Db	1886	----LSMDSPSD--LSPNAPPVG FENTA QFLEKLQQE-DRPSAEGSIDSSGF EKVDHE--	1936
Qy	563	MDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSS	622
		: : : :	
Db	1937	-----GLDEFAAPP-----VHDPMQKS VFGSLGSDDMKPGS	1967
Qy	623	SP-----LEASSVNYESIKHEPENPPP YEEAMS VSLKVSGIKEEIKEPENIN-----AAL	672
		: : : : : : :	
Db	1968	QDDGVFVIERNEAN-----EATLKKNQKMSSHNDVIEKNYFNDNAPT AAL	2013
Qy	673	QETEAPYISIACDLIKETKLSAEPAPDFS DYSEMA-----KVEQVPDPHSEL	719
		: : : : :	
Db	2014	--LESPIAEEARKLVQDAVESA-----SEYKKQAVDSGDEIGRELLDNVEQKIEQVKEP	2065
Qy	720	VEDSSPDSEPVDLFSDDISPDVPQKQDET VMLVKESLTETS FSMIEYENKEKLSALPPE	779
		: : : : : :	
Db	2066	IVDSL--HKAYDGVGDVFHETVPNAVDDFVREA EKQLPESPVPEKIE-----TPE	2113

Qy 780 G G K P Y L E S F K L S L D N T K D T L -- L P D E V S T L S K K E K I P L Q M E E L S T A V Y S N D D L F I S K E A Q 837
 | : || : : ||| : : | | | : | :
 Db 2114 ----- P L V D I H D T V D K V H D E V D N F L R R E P T P - P F E T D D V A P L S D D K P Q F G N Q T P 2161

Qy 838 I R E T E T F S D S S P I E I I D E F P T L I S S K T D S F S K L A R E Y T D L E V S H K S E I A N A P D G A G S L P C 897
 : || | : | : | : : : : : : | | : | : :
 Db 2162 E E D E T T F D R K G P L T I P E E V E K A A A A Q N N D L D --- D F D P L V T S N T G A A F G A A V G A A A A -- 2215

Qy 898 T E L P H D L S L K N I Q P K V E E K I S F S D D F S K N G S A T S K V L L L P P D V S A L G H T Q A E I E S I V K P K 957
 : : || : : : : : : : : : : : : : :
 Db 2216 ----- V E S L T E E E M ----- F G H -- Q K F E T V P R P P 2237

Qy 958 V L E K E A E K L P S D T E K E D R S P S A I F S A D L G ----- K T -- 989
 | | | | | : : : : : : : : : : : :
 Db 2238 T ----- P P K D I S D E D V K P S T V --- N L G P S H H H S H P S S P H H S I L K H H G D A W I D F K T V P 2286

Qy 990 - S V V D L L Y W R D I K K T G V V F G A S L F L L L S L T V F S I V S V T A Y I A L A L L S V T I S F R I Y K G V I Q 1048
 | : | : | | | | | : : | : : | : : : : | | | | : : : |
 Db 2287 P C V L D V I Y W R D A K K S A I V L S L A L L V L F V L A K Y P L L T V V T Y S L L L A L G A A G F R V F K K V E A 2346

Qy 1049 A I Q K S D E G H P F R A Y L E S E V A I S E E L V Q K Y S N S A L G H V N C T I K E L R R L F L V D D L V D S L K F A 1108
 | : | : | | | | : : : : | : : : | : : : | : : : | : : : |
 Db 2347 Q I K K T D S E H P F S E I L A Q D L T L P Q E K V H A Q A D V F V E H A T C I A N K L K K L V F V E S P L E S I K F G 2406

Qy 1109 V I M W V F T Y V G A L F N G L T L L I L A L I S L F S V P V I Y E R H Q A Q I D H Y L G L A N K N V K D A M A K I Q A 1168
 : : : | | : : | : | | | : : | | | : : | | : : : | : : : |
 Db 2407 L V L W S L T Y I A S W F S G F T L A I L G L L G V F S V P K V Y E S N Q E A I D P H L A T I S G H L K N V Q N I I D E 2466

Qy 1169 K I P G L K 1174
 | : | :
 Db 2467 K L P F L R 2472

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
 2586/2

Query Match 8.8%; Score 519.5; DB 2; Length 2607;
 Best Local Similarity 20.4%; Pred. No. 1.8e-13;
 Matches 292; Conservative 175; Mismatches 474; Indels 491; Gaps 55;

Qy	1	MEDLDQSQLVSSSDSPPRPQPAFKYQFVREPEDEEE-----EE	38
Db	1397	LEKVEVQP--DLSQNSPAPHKIIDLHF-NIPKDHEDYGNDYVFPFGTESSEESQKADGNQE	1453
Qy	39	EEEEED-----EDEDLEELEVLERKPA-----AGLSAAP-----	67
Db	1454	NQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDVDASDVNEQDEESTLKIL	1513
Qy	68	--VPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP--ERQPSW-----	108
Db	1514	KVVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV	1569
Qy	109	-----DPSPVSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW	159
Db	1570	TESEISEMAPQVSESTCPIPEPL-----ADLKLPVEDDEKTPEPEPVVPGQVQERIPIE	1624
Qy	160	TPPAPA-PAAPPSTP-----AAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQE---	208
Db	1625	VEQAPTIPQRPPRAPKSELPKVAKPLDDSKS-----RVRFAPLNIKLGRITYSEEQQKEL	1678
Qy	209	----DFPSVLLETAASXP-----SLSPLSAASFKEHEY--LGNLSTVLPTTEGTLQEN	254
Db	1679	VESLERPLTII-TQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMMDMQSVPHSPQEKQEE	1737
Qy	255	VSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVK--	312
Db	1738	I-EALSEIIEEPQAM-----KEVEKPVESAPEKDNESLEAPEIINEPIRRVLVETK	1787
Qy	313	-----NKDEEEKLVSNNILHXQQELPTALTCLVKEDDEVVSSEKAKDSFNEKRVAVEA	364
Db	1788	IMGPGKSLNEDNDDDDDGSECLDSIGDL-----SERTIQRFN---TSIDD	1829
Qy	365	P--MREEYADFKPFERVWEVKDSKED--SDMLAAGGKIESNLESKVDKCFADSLEQTNH	420
Db	1830	PSIRDSFSSISSFGDRQKFRTAIENIRQDLLPFQSSVSQYLRSNP--SQQLLVTNL	1886
Qy	421	EKDSESSNDDTSFPSTPEGI-----KDRSGA--YITCAPFNPAATESIATNIF	466
Db	1887	SMDSPS---DLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSIDSSGFEEKVDHEGLDEF	1943
Qy	467	PLLEDPTSEN-----XTDEKK-----IEEKKAQIVTEKNTSTKTSNPPFFVAAQDS	511
Db	1944	PPVHDPMQSKSVFGLSGDDMKPGSQDDGVFIERNEANEATLKNQKMSSHNDVIEKNY	2003
Qy	512	ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV-TGTKIAYE----TKMDLV	566
Db	2004	FNDNAPT---AALLESPIAEARKLVQDAVESASEYKKQAVDSGDEIGRELLDNVEQKIE	2060
Qy	567	QTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLE	626
Db	2061	QVKEPIVDLSLHKAYDGVGVFH-ETVNAV-DDFVREAE-----	2097
Qy	627	ASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAAALQETEAPYISACDL	686
Db	2098	-----KQLPESPVP-----EKIETPE-----PLVDIHDTV	2122

Qy 687 IK-----ETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSDIPDV 741
 | : | | | | : | : | : | : :
 Db 2123 DKVHDEVNDNFLRREPTPPFE-----TDDVAPLSDDKPQFGNQ----- 2160

Qy 742 PQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLP 801
 : | | | | | : | : | : | : | : | :
 Db 2161 -PEEDETTFDRKGPLT-----IP 2177

Qy 802 DEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDDSSPIEIIDFPTLIS 861
 : | | : | : | : | : | : | : | : | :
 Db 2178 EEV-----EKAAAAQNND-----LDDFDPLVT 2199

Qy 862 SKT-----DSFSKLAR-----EYTDLEVSHKSEIANAPD 890
 | | : | : | : | : | : | : | : | :
 Db 2200 SNTGAAFGAAVGAAAAVESLTEEEMFGHQKFETVPRPPTPPKDISDEDVK-PSTVNLGPS 2258

Qy 891 GAGSLPCTELPHD-----LSLKNIQPKVEEKIS-----FSDDFS 924
 | | : | : | : | : | : | : | : | :
 Db 2259 HHHSHPS--PHHSILKHHGDAWIDFKTVPPCAQNAFSPGEIMFLLAFFVYLSCFASFFS 2316

Qy 925 KNGSATSKVLLL-----PPDVSALG----- 944
 | : : | : | : | : | : | : | :
 Db 2317 KSLPLLDNLLSLVVYLSISLIHVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNI 2376

Qy 945 --HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKK 1002
 : : | | | | | : | | | : | : | : | :
 Db 2377 VLRVGLNVALVVGVAWSAHEAYKLTKS-----SGVLRKKEVLVDVIYWRDAKK 2423

Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1062
 : | : | : | : : : | | | | | : : | : | : | : | :
 Db 2424 SAIVLSLALLVLFVLAKYPLLTVTYSLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEI 2483

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVETVVGALFN 1122
 | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
 Db 2484 LAQDLTLPOEKVHAQADVFEHATCIANKLKLVFVESPLESIKFGVLVLSLTYIASWFS 2543

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 1174
 | | | | : : | | : | : | : : : | : | : | :
 Db 2544 GFTLAILGLLVGVSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 5.7%; Score 340.5; DB 2; Length 222;
Best Local Similarity 32.4%; Pred. No. 1.4e-07;
Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;

```
Qy      972 EKEDRSPSAIFSadL-GKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 1030
      :| : |: : : | || ::::| ||| :| :| | : ::| |
Db      9 KKYSKQPTWVPATDFPGK--ILDVIYWRDAKSAIVLSLALLLVLFVLAKYPLLTVVVTVYSL 66

Qy     1031 LALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIK 1090
      | |      ||::| | |::| | || | : : : | | : : : | |
Db     67 LLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFEHATCIAN 126

Qy     1091 ELRRLEFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 1150
      :|::| | : :::| | ::| || : : | | | : : ||| : || : | |
Db     127 KLKKLVFVESPLESIKFGLVLWSLTYYIASWFSGFTLAILGLLGVSVPKVYESNQEAIDP 186

Qy     1151 YLGLANKNVKDAMAKIQAKIPGLK 1174
      :| : ::| : | |::| :
Db     187 HLTATISGHLKKNVQNIIDEKLPFLR 210
```

RESULT 7

I38346

elastic titin - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I38346

R;Labeit, S.; Kolmerer, B.

Science 270, 293-296, 1995

A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.

A;Reference number: A57430; MUID:96026330; PMID:7569978

A;Accession: I38346

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-7962 <RES>

A;Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427

C;Genetics:

A;Gene: GDB:TTN

A;Cross-references: GDB:127867; OMIM:188840

A;Map position: 2q31-2q31

Query Match 5.6%; Score 331; DB 2; Length 7962;
Best Local Similarity 20.0%; Pred. No. 4.7e-05;
Matches 235; Conservative 144; Mismatches 404; Indels 392; Gaps 48;

```
Qy      32 EDEEEEEEEEEDEDEDLEELE--VLERK---PAAGLSAAPV-----PTAPA 73
      |:| ||||| | | |::| | |::| | : : | | | |
Db     6176 EEEREEEEEA EVTEYEVMEEP EYVVEEKLHIISKRV EAEPAE VTERQEKKIVLKP KIPA 6235

Qy      74 AGAPLMDFGNDFVPPAPRGPLPAAP-PVAPERQPSWDPSVPSSTVPAPSPLSAAAVSPSK 132
      : | : | || : ||:: | || | | | |
Db     6236 K-----IEEPPPAKVPEAPKKIVPEKK-----VPAPVP-KKEKVPPPK 6272
```

Qy 133 LPEDDEPPA---RPPP-----PPPASVS-----PQAEPVWTPPAPAPAAPPS-TPAA 175
 :||: : | : || | || | : | | | | : |
 Db 6273 VPEEPKKPVPEKKVPPKVIKMEELPAKVTEKHMQITQEEKVLVAVTKEAPPKARVPEE 6332
 Qy 176 PKRRGSSGAVVXXXXKIMDLK----EQPGNTISAGQEDF---PSVLLETAASXPS-LSPL 227
 ||| |:: || |:: :: : | : | : :
 Db 6333 PKR-----AVPEEKVLKLPKREEEPPAKVTEFRKRVVKEEKVSIEAPKREPQPIKEV 6385
 Qy 228 SAASFKEHEYLGNLSTVLPTEGTLQEN-VSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
 : || | |::| || :| |:: : | || | : |
 Db 6386 TIMEEKERAY-----TLEEEAVSVQREEEYEEYE----EYDYKEFEEYEPTTEE 6429
 Qy 287 GSSFS-----VSPKAESAVIV--ANPREEI 309
 : || | : : | | : :
 Db 6430 YDQYEEYEEERYERYEEHEEYITEPEKPIPVKPVPEEPVPTKPKAPPKVLKKAVPEEKV 6489
 Qy 310 IV----KNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAP 365
 | | | : ::: ::: :| | : | | || |
 Db 6490 PVPIPKKLKPPPPKVPPEEPKKVFEEKIHSITK--REKEQVTEPAAKVPMKPKRVVAEEK 6547
 Qy 366 MREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE 425
 : : | || | : : | : : | : : | : : |
 Db 6548 VVPRKEVAPPVRVPEVPKELEPEEV-----AFEEEVVTHVE-EYLVEEEEEEYIHEEE-E 6600
 Qy 426 SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSXTDEKKIEE 485
 : : | | : : | | | : : | | : : || ||
 Db 6601 FITEEEVVPVIPVKVPE-----VPRKPVPEEKKVPVPVKKKEAPPKVPPEVPKKPEE 6652
 Qy 486 KKAQIVTEKNTSTKTSNPPF-----VAAQDSETDYVTTDNL----- 521
 | : : | | | : : | : :
 Db 6653 KVPVLIPKKEKPPPAKVPEVPKKPVPEEKVPVPVKKVEAPPKVPPEVPKKPVPEKKVPV 6712
 Qy 522 -----TKVTEEVVANMPEGLTPDLVQEACESELNEVTGKIAIYETKMDLVQTSEV 571
 || | :|| | | : | : : | : || ||
 Db 6713 PAPKKVEAPPKVPPEVPKKLIPEEKKPTVPKKVEAPPPKVPKKREPVPVPVALPQEEEV 6772
 Qy 572 M-QESLYPAAQLCPSFEESEATP----- 593
 : : | : : | || | |
 Db 6773 LFEEIVPEEEVLP--EEEEVLPEEEVLPEEEVLPEEEIIPPEEEVPPEEEYVPEEE 6830
 Qy 594 -----SPVLPDIVMEAPLNSAVPSAGASVIQ-----PSSSPLEASSVNYESI- 635
 |||:: : | : : || | : | | : |
 Db 6831 EFVPEEEVLPEVKPKVPVPAPVPEIKKKVTEKKVIPKKEEAPPKVPPEVPKKVEEKRII 6890
 Qy 636 --KHE-----PENPPPYEEAMSVSLKVSGIKEEI---KEPENIN 669
 | | || || || || : : || |
 Db 6891 LPKEEEVLPEVTEEPPEEPISEEEIPEEPPSIEEV-----EEVAPPRVPEVIK 6939
 Qy 670 AALQETEAPYISIACDLIKETKLSAEPAPDFS DYSEMAKVEQVPDPHSELVEDSSPDSEP 729
 | : | | : | | || : : | : : |
 Db 6940 KAVPEAPTVP-----PKKVEAPP-----AKVSKKIPEEKVPVPVQKKEAPP 6980
 Qy 730 VDLFSDDSIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK 789
 : : || : | : || | | : || | :
 Db 6981 A-----KVPEVPKKVPEKKVLV-----PKKEAVPPAKGR----- 7009

Qy 790 LSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSP 849
 | : | : : | | : : | : | : | : :
 Db 7010 -----TVLEEKVSVAFRQEVVVKERLELEVVEAEVEE--IPEEEEFHEVEEYFEEGE 7059
 Qy 850 IEIIDEFPTLISSKTDSFSKLAREYTDLEV--SHKSEIANAPDGAGSLPCTELPHDLSLK 907
 : : | | : : : : : : | : : | : : | : :
 Db 7060 FHEVEEFIKLEQHRVEEHRVEKVHRVIEVFEAEVEVEFEKPKAPPKGP-----EISEK 7113
 Qy 908 NIQPK-----VEEKISFSDDFSNGSATS SKVLLLPDVSAL 943
 | | | | : : : : : : : : : :
 Db 7114 IIPPKKPPTKVVPKEPPAKVPEVPKKIVVEEKVRVPEE-----PRVPP----- 7157
 Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSP 978
 : : : : | | | | : : : : : : : :
 Db 7158 ----TKVPEVLPPK--EVVPEKKVPVPPAKKPEAP 7186

RESULT 8

T13564

microtubule-associated protein homolog - fruit fly (*Drosophila melanogaster*)

N;Alternate names: hypothetical protein EG:49E4.1

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13564

R;Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A;Reference number: Z17689

A;Accession: T13564

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5327 <SPA>

A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1

C;Genetics:

A;Cross-references: FlyBase:FBgn0025392

A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1

A;Note: EG:49E4.1

C;Superfamily: *Drosophila* 576K microtubule-associated protein homolog

Query Match 5.5%; Score 325.5; DB 2; Length 5327;
 Best Local Similarity 23.6%; Pred. No. 4.6e-05;
 Matches 275; Conservative 151; Mismatches 520; Indels 219; Gaps 53;

Qy 28 VREPEDEEEEEEEEE---DEDEDLEELVLERKPAAGLS-----AAPVPTAPAAAG 75
 : : : : | : : | : : | : : : : : : : : : : : :
 Db 1277 MEQVKDKEEHEQKIESGIITEKEAKKSASTPEEKETSDITSDDDELPAQLADPTTVPPKSA 1336
 Qy 76 APLMDFGNDFVPPA-----PRGPLPAAPPV-APERQPSWDPSPVSSSTVPAPSPLSAA 126
 | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 1337 KDREDTGSIESPPTIEEAIEVEVQAKQEAQKVPAPAEAAIKTEKSPLASK-ETSRPESAT 1395
 Qy 127 AVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPA-----APK 177
 : | | | : : : : : : : : : : : : : : : : : :
 Db 1396 ----GSVKEDTEQTKSKKSPVPSRPESEAKDKKSPFASGEASRPESVAESVKDEAGKAES 1451
 Qy 178 RRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----DFPSVLLETAASXP-SLSPLSA 229
 | | | : | | | : | | | | | : : |

Db 1452 RRESIAKTHKDESSLDKAKEQESRRESIAESIKPESGIDEKSALASKEASRPESVTDKS- 1510

Qy 230 ASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSS 289
 || : : | | | : ||| | : : | | | : :

Db 1511 ---KEPSRRESIAESLKAESTKDEKSAPPSKEASRPESVSVKDETEKSKEPSRRESIA 1567

Qy 290 FSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSN---ILHXQQELPTALTCLVKEDEVV 346
 | | | : | | : | | | | : : | : : | : :

Db 1568 ESAKPPIEFRE-VSRP-ESVIDGIKDESAKPESRRDSPLASKEASRPESVLESVKDEPIK 1625

Qy 347 SSEKAK-----DSFNEKRVAVE-APMREEYADFKPFFERVWEVKDS--KEDSDMLAAGGKI 398
 | : | : : : | : | : : : | : | : | : | : | :

Db 1626 STEKSRRRESVAESFKADSTKDEKSPLTSKDIS-RPESAVENVMDAPFKETS RPESAVGSM 1684

Qy 399 ESNLESKVDKKCFADSLEQTNHE--KDSESSNDDTSFP-STPEGIKDRSGAYITCAPFNP 455
 : || : | | : : : | | | | | | | | | |

Db 1685 KDESMSK-----EPSRRESVKDGAAQSRERSRPASVAESA--GADDLKELSRP 1732

Qy 456 AATE-----SIATNIFPLLEDPTS-----ENXTD--EKKIEEKKAQIVTEKN--TSTK 499
 : | : | : | : | : | | | | : : | | : | :

Db 1733 ESTTQSKEAGSIKDEKSPLASEEASRPASVAESVKDEAEKSKEESRRESVAEKSPLPSKE 1792

Qy 500 TSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMP----EGLTPDLVQEACESELNEVTGT 555
 | | | : | | | | | | | | | : : |

Db 1793 ASRPASVA--ESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDE-----AE 1845

Qy 556 KIAYETKMDLVQTSEVM--QESLYPAAQLCPSFEESEATPSPVLPDIVME-APLNSAVPS 612
 | | : : | : : | : : : : : : | | : | | |

Db 1846 KSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEAS 1905

Qy 613 AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEI---KEPENIN 669
 ||| : | | : : | : | : : | : | |

Db 1906 RPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRE 1965

Qy 670 AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEP 729
 : : : | | | | : | : | | | : | |

Db 1966 SVAEKSPLP-----SKEASRPASVAESIKDEAEKSKEE----SRRESVAEKSP---- 2009

Qy 730 VDLFSDDSIIPDVPQKQDETVMVLKESLTETSFESMIE--YENKEKLSALP-PEGGKP--Y 784
 : | : | | : : : | | | : : | | | | : |

Db 2010 -----LPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASV 2058

Qy 785 LESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQME-----LSTAVYSNDDLFIKAEQIRE 840
 | | | : : | : | | | | : | | | : | | |

Db 2059 AESIKDEAEKSK-----EESRRESAAEKSPLPSKEASRPASVAESVKDEADKSKEESRR- 2112

Qy 841 TETFSDDSPIEII--DEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT 898
 | : : | : | : | : : | : | | | : | | :

Db 2113 -ESMAESGKAQSIKGDQSPLKEVSRPES---VAESVKDDPVKSK-EPSRRESVAGSVTAD 2167

Qy 899 ELPHDLSLKNIQPKVEEK-----ISFSDDFSKNGSATSKVLLLPPDVSA LGHTQAE 949
 | : : | : | | : | | | : : :

Db 2168 -----SARDDQSPLESKGASRPESVVD SVKDEAEKQES-----RRESK 2205

Qy 950 IESIVKPKVLEKEAEKKL-----PSDTEKEDR-SPSAIFSADLGKTSVVDLLYW---RDI 1000
 | : : | : : | : : : : | : : | : : | |

Db 2206 TESVIPPKAKDDKSPKEVLQPVSM TETIREDADQPMKPSQAESRRESIAESIKASSPRDE 2265

Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407
: | : | | | | | : : : | |
Db 235 T---KPLAAAEFVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280
Qy 408 KKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467
| | : : | : | | | |
Db 281 -----ASTEPPV---AAATLTAPETPAL----- 301
Qy 468 LLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527
| : | | | | | | | |
Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320
Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579
| | : | : | : | | : | | : | | : | |
Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371
Qy 580 -AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHE 638
| | : : | : | | : : | : | | : | | : | | :
Db 372 PATLAVTDPDVTASAVPELPPVIAPSVPVSAVAETPVDLAPPVLPPVAAEPVPAVVAEET 431
Qy 639 PENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEP 697
| | | | : : : | : : | | : | | : | : : | |
Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVSTPPTTASVPETTAPPA 491
Qy 698 P-----DFSDYSEMAKVEQVPDPHSEL-----VEDSSPDSEPVDLFSDDSI--DVPQK 744
| | | | : | | | : | | : | | : | : |
Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDL 550
Qy 745 QDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEV 804
: | : : | : : : : | : : : : | : : : |
Db 551 LEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603
Qy 805 STLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDFPTLI 860
| : | | : : : : | | : | | | | | :
Db 604 SLATPTEPIPVAPVVIQEAVIDAV-----EVPVTETST---SIP-ETTVEFPEAV 649
Qy 861 SSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDL 906
: | | : | : : : | | | | : : :
Db 650 AEKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701
Qy 907 KNIQPKVEEKISFSDDFSKNGSATSKVLL---LP-----PDVSALG----- 944
| | | : : : : : : : : : : | : | |
Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760
Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLY 996
: | | : | | : | | : : : | | : | : | |
Db 761 ITAGDNPNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814
Qy 997 WRDIKKTGV 1005
| | : : | |
Db 815 -RDLQTTDV 822

RESULT 10
A47283
calphotin - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
 C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C;Accession: A47283
 R;Ballinger, D.G.; Xue, N.; Harshman, K.D.
 Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993
 A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and contains a leucine zipper.
 A;Reference number: A47283; MUID:93165730; PMID:8434015
 A;Contents: photoreceptor cells
 A;Accession: A47283
 A;Status: preliminary
 A;Molecule type: nucleic acid
 A;Residues: 1-873 <BAL>
 A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g157072
 A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124959)
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

Query Match 5.4%; Score 320.5; DB 2; Length 873;
 Best Local Similarity 22.5%; Pred. No. 6e-06;
 Matches 235; Conservative 122; Mismatches 367; Indels 321; Gaps 50;

```

Qy      59 PAAGLSAAPV-PTAPAAGAPLMDFGNDVFPAPRGPLPAAP----PVAPERQPSW-DPSP 112
      | :  ||| | |:| ||  ::  | ||  | |||  |||  |:  |
Db      9 PVSAPVAAPVTPSAVAAPVQVVSPA AVAVAPVAVAPAPAAPTAVTPVAP--PPTLASVQP 66

Qy     113 VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPP-----A 163
      : |||||:|:|:|:|:|  ||  | ||  | || |||
Db     67 ATVTVPAPAPIAAASVAP---VASVAPPVVAAPTTPA-----ASPVSTPPVAVAQIPVAV 118

Qy     164 PAPAAPP----STPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQEDFPSVLLET-- 217
      || |||  || ||  ::|  | |
Db     119 SAPVAPPVAATPTPVAP-----IPVAAPVIATPPVAASAPT 154

Qy     218 -AASXPSLSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLT 276
      || | :||: |  |:|  |  | |:  :  | ::  |
Db     155 PAAVTPVWSPVIAT-----PPVVPANTT----VPVAAPVAAPVAAVPVAVPVL 199

Qy     277 EFSELEYSEMGSFSVSPKAESAVIVAN-----PREEIIVKNKDEEEKLVSNILHXQQE 331
      :|:|  | :||  | || |
Db     200 P-----AVAPAV--APVVAETPAPPPVAEIPVAT----- 226

Qy     332 LPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDM 391
      :| :  |:| ||::  |  :| | | |  |  |
Db     227 IPECVAPLIPEVSVVAT---KPLAAAEPPVVAPPATET-----PVVAPAAASPH 272

Qy     392 LAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCA 451
      ::  :|: : : |  ||  :  : | :| |
Db     273 VSVAPAVETAVVAPVS-----ASTEPPV---AAATLTTA 303

Qy     452 PFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDS 511
      |  ||  | :| |  |||
Db     304 PETPAL-----APVVAESQ-----VAA--- 320

Qy     512 ETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEV 571
      |  |  | || :| :|  :| ||  :| ||  :| |
Db     321 -----NTVVATPPTPAPEPETIAPPV-----AETPEVASVAVA-ETTPPVV--PPV 364

```

Qy 572 MQESLYPA-----AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS 622
 ||: || | | : : |: | || :: |: || | : |
 Db 365 AAESI-PAPVVATTPVPATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVL 423

Qy 623 SPLEASSVNYESIKHEPENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYIS 681
 |: | | : || | | :: :| : : | | : | || :|
 Db 424 PPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVS 483

Qy 682 IACDLIKETKLSAEPAP-----DFSDYSEMAKVEQPVPDHSEL-----VEDSSPDSEPV 730
 : :| || | | || | :| || | : | | :|
 Db 484 TPPTTASVPETTAPPAAVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAE 542

Qy 731 DLFSDDSDIP--DVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788
 || : | :| ::| : |:: :| :|||
 Db 543 DLIIEPVEPPAPIPDLLLEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEV 595

Qy 789 KLSLDNTKDTLLPDEVSTLSKKEKIPLQ---MEELSTAVYSNDDLFISKEAQIRETETF 844
 :: : : | | : | ||:: :| | | : || |
 Db 596 AVAPITAPEPIPEPEPSLATPTEPIPVVEAPVVIQEAVDV-----EVPVTETST- 644

Qy 845 SDSSPIEIIIDEFPTLISSKTD SFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-- 901
 | | | ||| :: | | : | : : :|| || | ||:
 Db 645 --SIP-ETTVEFPEAVAQKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTP 693

Qy 902 -----HDLCLKNIQPKVEEKISFSDDFSKNGSATSQVLL----LP-----PDVS 941
 | :: | | | ::| : : : : : : :| :||
 Db 694 AVEIVTAAAEVSDTAIPLIDFPVPQEIAVA-EIPETETKPAEVIVEQSTIPIEAPVPEVS 752

Qy 942 ALG-----HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSA 980
 :| | :| | :| | :| : : |||
 Db 753 KYAEPVISEAPAAEVPITAGDNPNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD 811

Qy 981 IFSADLGKTSVVDLLYWRDIKKTGV 1005
 | : | : || ||: | |
 Db 812 --SVPVAK--ITPLL--RDLQTTDV 830

RESULT 11

T34418

hypothetical protein F12F3.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34418

R;Fulton, B.; Wohldmann, P.

submitted to the EMBL Data Library, July 1998

A;Description: The sequence of *C. elegans* cosmid F12F3.

A;Reference number: Z21521

A;Accession: T34418

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3488 <FUL>

A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3

A;Experimental source: strain Bristol N2; clone F12F3

C;Genetics:

A;Gene: CESP:F12F3.3

A;Map position: 5

A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1

Query Match 5.1%; Score 299.5; DB 2; Length 3488;
Best Local Similarity 20.6%; Pred. No. 0.0003;
Matches 272; Conservative 187; Mismatches 475; Indels 387; Gaps 57;

```
Qy      1 MEDLDQSPLV--SSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEV---- 54
          ::::| | ::      | : :| | : ::| | | :      | | : : |::|
Db      340 VDEVDDSTVLEEKKDDGDDKSKPKTKKKIIKKKETPESEQVTAAEPEQQKISEVDVQSVA 399

Qy      55 -----LERKPAA-----GLSAAPVPT-----APAAGA-----PLMD-----FGNDF 85
          ::|| |      || | :      | |      | |      | |
Db      400 ETEVGAKKKPDAEKPTDLSKAKKDSKSKKSDEPEASTEESTTEKPTNDKTSKKSAEKKT 459

Qy      86 VPPAPR---GPLPAAPPVAPERQPSWDPSPVSVSTVPA-----PSPLSAAAV 128
          | |      || | || : : | | | : |      | :| :
Db      460 VKPKKEVTGKPLEAKKPVEDKKDASQPSSSKESSPPTDGKKKKQIPKALFIPDEISSRFG 519

Qy     129 SPSKL-----PEDDEPPARPP--PPPPASVS-----PQAEPVWTPPPAP 164
          || :      :      | : | | |||      :|| : :
Db     520 DPSTMHSETNITTTIRGREGSADAKTPLVEPLSASVSMKVFTLVESAKEAEFSFKRRSE 579

Qy     165 AP-----AAPPSTPAAPK-----RRGSSGAVVXXXXKIMD----LKEQPGN----- 201
          |      ||: : |      : | :| : :      | :| : :| :
Db     580 TPDDKSRKKEGLPPAKKSEKKDEVTAEQSTEALIESKKKEVDESKISEQQPSDKNKSEV 639

Qy     202 ----TISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGNLSTVL---PTEGTLQEN 254
          :|| | |      |      | : : | : : | ||      : : : :
Db     640 VGVPEKAAGPETKKDV--SEIEEVPKKKTIKKKTEKSDSSISQKSNVLKPADDDKSKSDD 697

Qy     255 VSEASKEVSEKAKTLLID-----RDLTEFSELE-----YSEMGSSFSVSP 294
          |:: ||: :| :      |      | | : | |      :| || :|
Db     698 VTDKSKKTTEDQTKVATDSKLEKAADTTKQIETETVVDDKSKKKVLKKKTEKSDSF-ISQ 756

Qy     295 KAESAVIV--ANPRE----EIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKED----- 343
          |:: :| | | :| || :::| | :| : :| | | : |
Db     757 KSETPPVVEPTKPAESEAQKIAEVNKAKKQKEVDDNL---KREA EVAAKKIAD EKLKIEA 813

Qy     344 -----EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG 395
          || ::::| | : : : : | : : | : :| : | |
Db     814 EANIKKTAEEVAACKQKEKDEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEAD---AVK 870

Qy     396 GKIESNLESKVD--KKCFAD--SLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCA 451
          : | | ::::| | || || ||: : | : | : | | | :|
Db     871 KQKELNEKNKLEAAKKSADKLKLEESAAKSKKVSEESVKF---GEEKTKAGEKTVQV 927

Qy     452 PFNPAATESIATNIFPLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDS 511
          | : ::| | | | | | :||| :|| ||| :| :      :| |
Db     928 ESEPTSKKTIDTKDVGATE-PADE--TPKKKI IKKK----TEKSDSS-----ISQKS 972

Qy     512 ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTK-----IAYETKMDL 565
          || : : :| | :      | : || :| : : | |      || :|| :
Db     973 ATD---SEKVSQKEQDEPTKPAVSETQMVT EADKSKKQKETDEKLKLD AEIAAKTKQEA 1029

Qy     566 VQTSEV-MQESLYPAAQLCPSFESEATPSPVLDP-IVMEAPLNSAVPSAGASVIQPSSS 623
          : |:: || : :      | : | | : :| : : : || : : :
Db    1030 DEKSKLDAQEKIKKVS-----EDDAARKEKELNDKLKLESEIATKKASADKLKLEEQAQ 1083
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A;Residues: 1-3924 <CHA>
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
 R;Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins
 reveal a family of alternatively spliced genes.
 A;Reference number: A39643; MUID:91302466; PMID:1830053
 A;Accession: A39643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2077 <OT1>
 A;Cross-references: GB:X56957
 A;Accession: B39643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1443,3585-3924 <OTT>
 A;Cross-references: EMBL:X56958
 R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux,
 S.E.; Ward, D.C.; Forget, B.G.
 Genomics 10, 858-866, 1991
 A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin
 gene.
 A;Reference number: A40334; MUID:92009921; PMID:1833308
 A;Accession: A40334
 A;Molecule type: DNA
 A;Residues: 463-474,'PE',477-495 <TSE>
 A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
 R;Chan, W.; Kordeli, E.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993
 A;Title: 440-kD ankyrinB: structure of the major developmentally regulated
 domain and selective localization in unmyelinated axons.
 A;Reference number: A49462; MUID:94075409; PMID:8253844
 A;Accession: A49462
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
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 A;Cross-references: GDB:127607; OMIM:106410
 A;Map position: 4q25-4q27
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 C;Keywords: alternative splicing
 F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
 F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
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 F;96-128/Domain: ankyrin repeat homology <AN02>
 F;129-161/Domain: ankyrin repeat homology <AN03>
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 F;191-223/Domain: ankyrin repeat homology <AN05>
 F;232-264/Domain: ankyrin repeat homology <AN06>
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 F;298-330/Domain: ankyrin repeat homology <AN08>
 F;331-363/Domain: ankyrin repeat homology <AN09>
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 F;397-429/Domain: ankyrin repeat homology <AN11>
 F;430-462/Domain: ankyrin repeat homology <AN12>

F;463-495/Domain: ankyrin repeat homology <AN13>
 F;496-528/Domain: ankyrin repeat homology <AN14>
 F;529-561/Domain: ankyrin repeat homology <AN15>
 F;562-594/Domain: ankyrin repeat homology <AN16>
 F;595-627/Domain: ankyrin repeat homology <AN17>
 F;628-660/Domain: ankyrin repeat homology <AN18>
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 F;694-726/Domain: ankyrin repeat homology <AN20>
 F;727-759/Domain: ankyrin repeat homology <AN21>
 F;760-792/Domain: ankyrin repeat homology <AN22>
 F;793-825/Domain: ankyrin repeat homology <AN23>

Query Match 5.0%; Score 299; DB 2; Length 3924;
 Best Local Similarity 21.5%; Pred. No. 0.00037;
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

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Qy      14 DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK 58
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Db      1648 DIPDETQSTQKQHKPSLGIKKPVRRKLKEKQKQKEEGLQASAEKAELKKGSSEESLGED 1707

Qy      59 PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----- 92
      | ||:  |:||  |      :||::
Db      1708 P--GLAPEPLPTVKAT--SPLIEETPIGSIKDKVKALQKRVEDEQKGRSKLPIRVKGKEDV 1764

Qy      93 -----PLPAA-PPVAPERQPSWDPSP-----VSSTVPAPSPL 123
      | |||  | :  ||      |||      ||      ||:
Db      1765 PKKTTHRPHPAASPSLKSERHAPGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV 1824

Qy     124 SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW 159
      | :|      ||||  |      | :      | ||  |:  :  ||
Db     1825 SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSTKTERHPPVSPSGKTDKRPPV- 1883

Qy     160 TPPAPAPAAPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPNGTISAGQEDFPSVLLE 216
      :|      || :|      ::|      ||      | || :|      : :  |
Db     1884 SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLVPVSPSG 1934

Qy     217 TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT 268
      | :||  |      :|      :  |      :      :  | |:  |      |:  || |
Db     1935 KTEKQPPVSPTS KTERIEETMSVRELMKAFQSGQDPSKHKTGLFEHKSQKQKQPEKGKV 1994

Qy     269 -----LLIDRDLTEFSELEYSEMGSFSVSPKAES--AVIVANPREEIIVKNKDE-- 316
      :|  |:  : :|  :  :  |      |:  |||  | |:  :  | || :|
Db     1995 RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAESKRGVRVSS----IGVKKEDAAG 2049

Qy     317 -EEKLVSNNI-----LHXQQELPTALTCLVKE-----DEVV 346
      :||::|:  |      | :  |:|  |      | :  |      ||:
Db     2050 GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGMDLQISPDRKTSTDFSEVI 2107

Qy     347 SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED----- 388
      | :  | : : |:  |      : :  |      ||      : :  |: :
Db     2108 KQELEDNDKYQQFRLSEETEKALHLQVLTSPFNTTFPLDYMKDEFLPALSLQSGALDG 2167

Qy     389 -SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDSSESNDDTSFPSTPEGIKDRS 444
      |:  |  |  |  | : :      | |  ||      :  |:  | :  ||  |:  : ::
Db     2168 SSES LKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT 2225

Qy     445 GAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPF 504

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      |      :      | |      | |::: |      | | : : | |:::
Db      2226 G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTEDSETSTESFQKE 2277

Qy      505 FVAAQDSETDYVTTDNLTKVTEEVVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKM 563
      : |      | : |      : |      | | |      : | |      | : | : |
Db      2278 ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT---EEAACDEGQRTFGSS-AHKT-- 2330

Qy      564 DLVQTSEVMQESLYPAAQLCPSEFESEATPSPVL-----PDIVMEAP--LNSAV 610
      | |      | | |      : : | : | |      | | : : | | | :
Db      2331 ---QTDSEAQES-----TATSDETKALPLPEASVKTDGTESKPQGVIRSPQGLELAL 2380

Qy      611 PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVSG 657
      | | : | :      | | | | : : | : | : | | : | : | : |
Db      2381 PSRDSEVL SAVADDSLAVSHKDSLEASPVLEDNSSHKTPDSLEPSPLKESPCRDSLESSP 2440

Qy      658 IKEEIKE---PEN--INAALQETE--APYISACDLIKETKLSAEPAPDFSDYSEMAKVE 710
      : : : | : : : | : : | : | : | : | : | : | : |
Db      2441 VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE 2490

Qy      711 QPVPDHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI 765
      | : | : | | | : : | : | : | : | : | : |
Db      2491 Q-----TSLMESSGKSPLSPDTPSSEEVSYEVTPKTTDVSTPKPAVIHECAEED----- 2539

Qy      766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK----EKIPLQMEELS 821
      : | | | | | | | | : | : | : | : | : | | | |
Db      2540 DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAQKRDYKKEPKQEESSS 2589

Qy      822 TAVYSNDDLFIKSEA-QIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVS 880
      : | : | : : : | : | : | : | : | : | : | :
Db      2590 S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSESRKVSSSSSES----- 2633

Qy      881 HKSEIANAPDGAGS-----LPCTELPHDLSLKN-----IQPKVEEKISF--SDD 922
      : | : | | | | : | : | : : | | : : | : | :
Db      2634 -EPQLAQLKKGADSGLLPEPVIRVQPPSPLPSSMDSNSSPEEVQFQPVVSKQYTFKM NED 2692

Qy      923 FSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPD-----TEKEDRS 977
      : : : : | : | : | | | |
Db      2693 TQEEP GKSEE-----EKDSESHLAEDRHAVSTEAEDRS 2725

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RESULT 13

T16251

hypothetical protein F35A5.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

C;Accession: T16251

R;Leimbach, D.

submitted to the EMBL Data Library, January 1996

A;Description: The sequence of *C. elegans* cosmid F35A5.

A;Reference number: Z18485

A;Accession: T16251

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1274 <LEI>

A;Cross-references: EMBL:U46675; NID:g1166613; PID:g1166621; PIDN:AAB52641.1;

GSPDB:GN00028; CESP:F35A5.1

A;Experimental source: strain Bristol N2; clone F35A5

C;Genetics:
A;Gene: CESP:F35A5.1
A;Map position: X
A;Introns: 1272/2

Query Match 4.9%; Score 290.5; DB 2; Length 1274;
Best Local Similarity 20.5%; Pred. No. 0.00017;
Matches 221; Conservative 126; Mismatches 417; Indels 313; Gaps 45;

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Qy      71 APAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSP 130
      |: ||| | :| || : | | |: || |
Db     57 VSPSGAP-----SPVPIKNPVKKWKAPWEDDEPMEEAPAAP-----VP 94

Qy     131 SKLPEDDEP---PARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVX 187
      :| | | ||:| | : : | || || || :
Db     95 AKKVRDPSPKKVPAPKPRDASPKKIMAAKK----EPETLPAVPP-TPVKNPVKKFKAPWED 149

Qy     188 XXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP-SLSPLSAASFKEHEYLGNLSTVLP 246
      : |:|: | |: | : ||: | || || |||: : | |
Db    150 DEVDVDVKDAP--TVPAKKTPVLKKKEPAAAAKPRDPSPKKAAPSKEHDPI-----VPP 202

Qy     247 TEGTLQENVSEASKEVSEKAKTLLIDRDL--TEFSELE-----YSEMGSSFSVSPKA 296
      | | :| | | :| | | | : | || | :
Db    203 T-----PIKNPAKKWKPPWEDDEVPTTEEIKEPEPATRKVPALKKKKEPSTSVKPV 252

Qy     297 ESAVIVANPREEIIVKNKDE-----EEKLVSNNILHXQQELPTALT 339
      : : :| :| | :| : : : :| :
Db    253 D-----PSPTKKVPVKKEPEVPPTPIKNPTKKWKPPWEDETPVEEV--KEPPVPEKKAPV 305

Qy     340 VKEDVVSSEKAKDSFNEKR-----VAVEAPMREEYADFKPFERVWEVKDSKEDS 389
      :|: : : ||:| | | :| : || ||| | :
Db    306 LKKKDPAPAAKARDPSPSKAAPKKVEPSSPVVPPTPVKNPVKKYKP---PWEVDDEPAE- 361

Qy     390 DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYIT 449
      | | :|| | :| | | :| :| | :
Db    362 -----EVKKPSAPEKK--TPVLKRKEPEPSSTPSSDPSPKKAAPAVKPRDSSPKK 410

Qy     450 CAPF--NPAATESIATNIFLLEDPTSE-----NXTDEKKIEE-KKAQIVTEKNTSTKTS 501
      | :| | | | : :| : || :|| |: : | |
Db    411 ATPLQADPKAQEVPTPV----KNPVKKYKPPWEVDDEDPVVEEVKQPEAPAKKTPVLKRK 466

Qy     502 NPFFVAAQDSETDYVTNDLTKVTEEVVANMPE-----GLTPDLVQ---- 542
      | ||:| | | | | || || |
Db    467 EP---AAKD-----TAKPATSKTPET----PEKKDPVKPRDSSPKKVAAPKPSAQAPAT 513

Qy     543 -----EACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEES 589
      | | : :|: | :| : :|| | | :
Db    514 PVKNPVKKWRPPWEDDETADDVSKPTDAKKTPSLAKKDPAPAKESLKPADTKAPAKPR 573

Qy     590 EATPSPVLPDIVMEAPLSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAM 649
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		: : : : : : : :	
Db	624	AKPVPKTEVAPAAVKKPEPISKPKDTAPKKAEPNSPVV-----PPTP----	665
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFE	762
		: : : : : : :	
Db	666	-----VKNPVKKKWKP PWEDDDAPAKPVSL-----PEPEKKT PVLAKKAPTKPDSE	710
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
		:	
Db	711	-----AAADPVSGP-----	719
Qy	823	AVYSNDDL FISKEAQIRETETFS DSSPIEII-----DEFPTLISSKTDSFSKLAREYT	875
		: : : : : : : : : : :	
Db	720	---SSKDKPLAKKAPVKP---RDPSPMKAVPIKPAPKTEVPPAVVKKPEPVAK-----	766
Qy	876	DLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE-----EKISFSDDFSKNGSA	929
		: : : : : : : :	
Db	767	SRDPSPKK--AKAEPNSPVVPPT--PVKNPVKKWKP PWEDDDAPAEPVNVPEPEKKT PVL	822
Qy	930	TSKVLLLPDPVS-----ALGHTQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSP	978
		: : : : :	
Db	823	AKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKKPEPVSKPKE---PSPKKAEPNSP	876

Qy 148 PASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ 207
 |: : | | || :| : | | |
 Db 1012 TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNREETESPSQ 1055

Qy 208 E-----DFPSVLLETAASXP---SLSPLSAASFKE---HEYLGNLSTVLPTEGTLQENV 255
 | : | | | : | | : :| : ||: | : :
 Db 1056 EFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEEDKF 1115

Qy 256 SEAS-----KEVSEK-----AKTLLIDRDLTE 277
 |::: |::: || | :| :
 Db 1116 SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPPIEKTPLGERSV-N 1174

Qy 278 FS----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIIVKNK----- 314
 || |:: | | : : || | ||: | :| | |:: : :
 Db 1175 FSLTPNEIKASAEGEATAVVSPGVTQAVVEEHCASPEEKTLEVVSQSVTGSAGHTPY 1234

Qy 315 ----DEEEKLVSNILHXQQELPTALTCLVKEDEVVSSE--KAKDSFNEKRVAVEAPMRE 368
 ||: : : | :| || | :|| | | : : || |
 Db 1235 QSPTDEKSSHLPTTEVTENAQAVP-----VSFEFTEAKDE-NER--SSISPMDE 1279

Qy 369 EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDKKCFADSL 415
 | : | |:: : : || : | | : || | | : | :|
 Db 1280 PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPFEGKNGKQGFSD-- 1337

Qy 416 EQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNP---AATESIATNIFPLLED- 471
 | :| | | || : : | :| | :| | : : | :|
 Db 1338 -----KESPVS-DLTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE 1390

Qy 472 -----PTSENXTDEKKIEEKKAIQVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT 523
 || : : : | :|| | :| | :| :| : :
 Db 1391 RKLGGDGSPTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS 1447

Qy 524 VTEEVVA--NMPEGLTPDLVQEACESELNEVTGKTIAYETKMDLVQTSEVMQES-LYPAA 580
 | : || : || | | : :|| : : : ||| ||: : | :
 Db 1448 VSTASVATSSFPPTDD-VSPSLHAEVGSHPHSTEVDDSLSVSVVQTPTTFQETEMSPSK 1506

Qy 581 QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P 611
 : || : : | : : | :| :| |
 Db 1507 EECPRMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRSQSPDHP 1566

Qy 612 SAGASVIQ----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG 657
 : || : : | : | : | : | | | : ||| : : |
 Db 1567 TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPPTTEPSYTDNDLSELISVSQVEASP 1626

Qy 658 IKEEIKEPENINAALQETE-----APYISACDLIKE---TKLSAEP----- 696
 | | : ||| : | | : : || :
 Db 1627 STSSAHTPSQIASPLQEDTLSDVPPRDMSLYASLASEKVQSLEGEKLSPKSDISPLTPR 1686

Qy 697 -----APDFSDYSEMAK-----VEQVPDPHSELVEDS----- 723
 : | ||| : || : | | : : | :
 Db 1687 ESSPTYSPGFSSTSGAKESTAAYQTSSSPIDAAAAEPYGRSSMLFDTMQHHLALSRLD 1746

Qy 724 -----SPDSEPVDLFSDD---SIPDVP---QKQD 746
 ||| | | : || :| :
 Db 1747 LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHVGGYYYEYKTE 1806

Qy 747 ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD 797


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      | :      | | : | :      | | : | | | |      : ::
Db      1807 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTTRTPEEGGYSY-----EISEK 1858

Qy      798 TLLPDEVs--TLskKEKIPLQMEELSTAVYSNDD-----LFISKEA 836
      |   | | | | | | :      : :: |      : |      | :
Db      1859 TTRTPEVSGYTYEKTERSRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 1918

Qy      837 QIRETETFSdSSP-----IEIIDEFPTLISSKTDSFskLAREYT-----DL 877
      | | | : | |      | ::      : | | :      | |      | |
Db      1919 YSYETTTKTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 1978

Qy      878 -----EVSH-KSEIANA---PDG-----AGSLPCTELPHDLsLKNIQP-----KV 913
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Db      1979 CLVSSCEfKHPKTELSPSFINPNPLEWFAGEEPTeesERPLTQSGGAPPPSGGKQQGRQC 2038

Qy      914 EEKISfSDDfSKNGSATSkvLLLLPPDVsalGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970
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Qy      971 -----TEKEDRSPS-----AIFSADLGKTSVVDLLYWRDIKKTG 1004
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Db      2089 VTYKHMDPPPAPMQDRSPSPRHDPVSMVDPEALAIeqNLGKALKKDLKEKAKTKKPG 2145

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RESULT 15

QRMSP1

microtubule-associated protein MAP1B - mouse

N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein MAP1.2; microtubule-associated protein MAP5

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000

C;Accession: S07549; S44387; A33645

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2 and tau.

A;Reference number: A33645; MUID:90094539; PMID:2480963

A;Accession: S07549

A;Molecule type: mRNA

A;Residues: 1-2464 <NOB>

A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000

R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.

Arch. Biochem. Biophys. 310, 428-432, 1994

A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A;Reference number: S44387; MUID:94234720; PMID:8179328

A;Accession: S44387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 653-663,'IC' <SAN>

C;Superfamily: microtubule-associated protein MAP1B

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <MTB>

F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-694,695-698,699-702,708-711,712-715,716-719,720-723,727-730,758-761,764-767,783-786/Region: 4-residue repeats (K/R-K-E/D-X)

F;1861-2064/Region: 17-residue repeats

F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: phosphate (Ser) (covalent) #status predicted
F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (covalent) #status predicted
F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 289; DB 1; Length 2464;
Best Local Similarity 19.8%; Pred. No. 0.0005;
Matches 262; Conservative 148; Mismatches 474; Indels 442; Gaps 55;

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Qy      32 EDEEEEEEEEEDEDEDL-EELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAP 90
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Db    1009 EAEQSEEEGEEEDKAEDAREEGYEPDKTEADYVMAVADKAAEAGVTEEQYGY----- 1061

Qy      91 RGPLPAAPPV-APERQPSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPA 149
      | | : : | | : | | | : | | | | : | | |
Db    1062 LGTSAKQPGIQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTA 1112

Qy     150 SVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED 209
      : : | | ||| : | : | | |
Db    1113 TSGYTQSTIEISSEPTPMDEMSTP-----RDVMSDETNNNEETESPSQEF 1156

Qy     210 FPSVLLETAASXPSLSPLSAASFK-----EHEYLGNLSTVLPTEGTLQENVSE 257
      | : : | : ||| : | : || : | : : | :
Db    1157 VNITKYESSLYSQEYSKPAVASFENGLSEGSKTDATDGKDYNASASTISPPSSMEEDKFSK 1216

Qy     258 AS-----KEVSEK-----AKTLLIDRDLTEFS 279
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Db    1217 SALRDAYCSEEKELKASAELDIKDVSDERLSPAKSPSLSPSPSPSPPIEKTPLGERSV-NFS 1275

Qy     280 ----ELEYSEMGSFSVSPKAESAVI---VANPRE---EIIVKNK----- 314
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Db    1276 LTPNEIKVSAEGEARSVSPGVQTQAVVEEHCASPEEKTLEVVSQSQSVTGSAGHTPYQSP 1335

Qy     315 -DEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADF 373
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Db    1336 TDEKSSHLPTEVSENAQAVPVSF-----EFSEAKDE-NER--ASLSPMDEPVPDS 1382

Qy     374 K-PFERVWE-----VKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE 425
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Db    1383 ESPVEKVLSPLRSPPLLGSSEPYEDFLSADSKVLGR-----RSESPFE 1425

Qy     426 SSNDTSFSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXT----- 478
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Db    1426 GKNGKQGFPDRESPVSD-----LTSTGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS 1480

Qy     479 -----DEKKI-----EKKKAQIVTEKNTSTKTSNPPFFVAAQDSETD 514
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Db    1481 SQSALALDERKLGSDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDT 1538

Qy     515 YVTTDNLTKVTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVM 572
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Db    1539 YSHMEGVASVSTASVATSSSFPEPTTDD-VSPSLHAEVGSHPHSTEVDSDLVSVVQTPTTF 1597

Qy     573 QES-LYPAAQLCP-----SFESEATPSPVLPDIVMEAPLNSAV-- 610
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Db    1598 QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD 1657
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Qy 611 -----PSAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAM 649
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 Db 1658 FSRQSPDHPTLGASVLHITENGPTVDYSPCDIQDSSLSHKIPPTTEEPSYTQDNDLSELI 1717

Qy 650 SVS-LKVSGIKEEIKEPENINAALQETE-----APYISIACDLIKE---TKLSAE 695
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 Db 1718 SVSQVEASPSTSSAHTPSQIASPLQEDTLSDVVPREMSLYASLASEKVQSLEGEKLSPK 1777

Qy 696 P-----APDFSDYSEMAK-----VEQPVPDHSELVEDS- 723
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 Db 1778 SDISPLTPRESSPLYSPGFS DSTSAAKETAAAHQASSSPPIDAATAEPYGRSSMLFDTM 1837

Qy 724 -----SPDSEPVDLFSD-----DS 737
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 Db 1838 QHHLALNRDLTTSSVEKDSGGKTPGDFNYAYQKPENAAGSPDEEDYDYESQEK TIRTHDV 1897

Qy 738 IPDVPQKQDETVMML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788
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 Db 1898 VRYYYEKTERTIKSPCDSGYSYETIEKTTKTPEDGGYTCEITEKTRTPEEGGYSY---- 1953

Qy 789 KLSLDNTKDTLLPDEVS--TLSKKEKIPLQMEELSTAVYSNDD----- 829
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 Db 1954 ----EISEKTTRTPEVSGYTYEKTERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEK 2009

Qy 830 --LFISKEAQIRETETFS DSSP-----IEIIDEFPTLISSKTDSFSKLAREYT----- 875
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 Db 2010 ITSFPESSESYSYETSTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTTEKKSP 2069

Qy 876 -----DL-----EVSH-KSEIANA---PDG----AGSLPCTELPHDLSLKNIQP--- 911
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 Db 2070 SEARQDVDLCLVSSCEFKHPKTELSPSFINPNPLEWFAGEEPTEESEKPLTQSGGAPPPS 2129

Qy 912 -----KVEEKISFSDDFS KNGSATS KVL LLLPPDV SALGHTQAEIESIVKPKVLEKEAE 964
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 Db 2130 GKGQQGRQCDETPP TSVSESAPSQTDS DV---PPETE-----ECPSITADANIDSEDE 2179

Qy 965 KK-LPSD-----TEKEDRSPS-----AIFSADLGKTSVVDLLYWR 998
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Qy 999 DIKKTG 1004
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 Db 2240 KTKKPG 2245

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 Job time : 38.1547 secs

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:09:02 ; Search time 116.281 Seconds
(without alignments)
3191.803 Million cell updates/sec

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Perfect score: 5923
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Scoring table: BLOSUM62
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Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	5815	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
2	5815	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
3	5815	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
4	5810	98.1	1192	9	US-09-789-386-2	Sequence 2, Appli
5	5810	98.1	1192	9	US-09-893-348-23	Sequence 23, Appl
6	5810	98.1	1192	12	US-10-267-502-429	Sequence 429, App
7	5810	98.1	1192	16	US-10-327-213-9	Sequence 9, Appli
8	5810	98.1	1192	16	US-10-466-258-9	Sequence 9, Appli
9	5794	97.8	1192	12	US-10-408-967-7	Sequence 7, Appli
10	4296.5	72.5	1163	9	US-09-893-348-18	Sequence 18, Appl
11	4277.5	72.2	1163	12	US-10-267-502-431	Sequence 431, App
12	1495.5	25.2	373	9	US-09-789-386-6	Sequence 6, Appli
13	1495.5	25.2	373	9	US-09-765-205-6	Sequence 6, Appli
14	1495.5	25.2	373	9	US-09-893-348-24	Sequence 24, Appl
15	1495.5	25.2	373	12	US-10-408-967-8	Sequence 8, Appli
16	1495.5	25.2	373	14	US-10-060-036-72	Sequence 72, Appl
17	1487.5	25.1	373	16	US-10-466-258-4	Sequence 4, Appli
18	1417	23.9	289	9	US-09-789-386-4	Sequence 4, Appli
19	1225.5	20.7	379	14	US-10-205-194-164	Sequence 164, App
20	1187	20.0	360	9	US-09-893-348-20	Sequence 20, Appl
21	931	15.7	199	9	US-09-893-348-25	Sequence 25, Appl
22	931	15.7	199	12	US-10-660-946-1	Sequence 1, Appli
23	924	15.6	199	12	US-10-408-967-9	Sequence 9, Appli
24	922	15.6	199	12	US-09-978-360A-467	Sequence 467, App
25	908	15.3	199	9	US-09-893-348-21	Sequence 21, Appl
26	890	15.0	199	16	US-10-466-258-11	Sequence 11, Appl
27	791	13.4	777	14	US-10-205-219-93	Sequence 93, Appl
28	787.5	13.3	776	12	US-10-660-946-5	Sequence 5, Appli
29	787.5	13.3	776	12	US-10-267-502-430	Sequence 430, App
30	779	13.2	780	12	US-10-267-502-432	Sequence 432, App
31	705	11.9	356	12	US-10-660-946-6	Sequence 6, Appli
32	704	11.9	593	15	US-10-108-260A-2892	Sequence 2892, Ap
33	688	11.6	208	12	US-10-660-946-7	Sequence 7, Appli
34	671	11.3	267	12	US-10-660-946-8	Sequence 8, Appli
35	671	11.3	267	14	US-10-205-194-127	Sequence 127, App
36	630	10.6	266	12	US-10-276-774-2330	Sequence 2330, Ap
37	625.5	10.6	236	9	US-09-729-674-20	Sequence 20, Appl
38	625.5	10.6	236	9	US-09-765-205-26	Sequence 26, Appl
39	625.5	10.6	236	12	US-10-408-967-2	Sequence 2, Appli
40	625.5	10.6	269	14	US-10-106-698-6222	Sequence 6222, Ap
41	541.5	9.1	168	10	US-09-809-391-563	Sequence 563, App
42	541.5	9.1	168	10	US-09-882-171-563	Sequence 563, App
43	541.5	9.1	168	12	US-10-164-861-563	Sequence 563, App
44	520	8.8	222	12	US-10-267-502-428	Sequence 428, App
45	513	8.7	241	12	US-10-660-946-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

Db 481 PLLGDPTSENKTDEKKIEEKKAIQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE 540

Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
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RESULT 2

US-09-972-599A-6

; Sequence 6, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

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; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
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; ORGANISM: Homo sapiens
US-09-972-599A-6

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Query Match          98.2%; Score 5815; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 5.8e-284;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
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Qy    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVV 346
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Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
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Qy    467 PLLEDPTSSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 526
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Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
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 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE 705
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 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE 720
 Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 765
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 780
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840
 Qy 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAALGH 945
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAALGH 959
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAELGKTSVVDLLYWRDIKKTGV 1005
 |||||||||||| ||||||||||||||||||||:| ||||||||||||||||
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELGKTSVVDLLYWRDIKKTGV 1019
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 3

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71

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Query Match          98.2%; Score 5815; DB 14; Length 1192;
Best Local Similarity 97.2%; Pred. No. 5.8e-284;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDSPVSTVPAP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDSPVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
        |||:          |:      : ||||||||||||||||||||||||||||
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480

Qy    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 526
        ||| ||||| |||||||||||||||||||||||||||| ||||||||||||||||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 540

Qy    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF 586
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF 600

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Qy 587 EESEATPSVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 646
 Db 601 EESEATPSVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660

Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 705
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 720

Qy 706 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 765
 Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 780

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSESKLAREYTDLEVSHKSEI 885
 Db 841 SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSESKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGH 945
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA- 959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSALSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLT 1125
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLT 1139

Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 4

US-09-789-386-2

; Sequence 2, Application US/09789386
 ; Patent No. US20020010324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MICHALOVICH, DAVID
 ; APPLICANT: PRINJHA, RABINDER KUMAR
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30165-C1
 ; CURRENT APPLICATION NUMBER: US/09/789,386
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR APPLICATION NUMBER: US 09/359,208

; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match 98.1%; Score 5810; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 1e-283;
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180

QY    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:          |:          : ||||||||||||||||||||||||||||
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

QY    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

QY    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV 346
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

QY    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

QY    407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

QY    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE 526
      ||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540

QY    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

QY    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660
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; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: IL 124500
 ; PRIOR FILING DATE: 1998-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-893-348-23

Query Match 98.1%; Score 5810; DB 9; Length 1192;
 Best Local Similarity 97.2%; Pred. No. 1e-283;
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

QY	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
QY	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
QY	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRRG	180
QY	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSLSP	226
		: : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSLSP	240
QY	227	LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
QY	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
QY	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
QY	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
QY	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
QY	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
QY	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646

Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPPYE 660
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 705
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 720
 Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 765
 Db 721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 780
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840
 Qy 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGH 945
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA- 959
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSALSKTSVVDLLYWRDIKKTGV 1019
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGFALFNGLT 1125
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGFALFNGLT 1139
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 6

US-10-267-502-429

; Sequence 429, Application US/10267502

; Publication No. US20040071700A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob

; APPLICANT: Galant, Ron

; TITLE OF INVENTION: Obesity Linked Genes

; FILE REFERENCE: LSD-07416

; CURRENT APPLICATION NUMBER: US/10/267,502

; CURRENT FILING DATE: 2003-01-27

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 429

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-267-502-429

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS SKVLLLPDVSALGH 945
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS SKVLLLPDVSALA- 959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSTDEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLES 1065
 Db 1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139

Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 7

US-10-327-213-9

; Sequence 9, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-327-213-9

Query Match 98.1%; Score 5810; DB 16; Length 1192;

Best Local Similarity 97.2%; Pred. No. 1e-283;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 Db 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKASAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKASAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKESQIRETETFSOSSPIEIIIDEFPTLISSKTDSFSLKAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKESQIRETETFSOSSPIEIIIDEFPTLISSKTDSFSLKAREYTDLEVSHKSEI	900

QY 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH 945
 |||
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA- 959
 QY 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
 |||:|
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSaelSKTSVVDLLYWRDIKKTGV 1019
 QY 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
 |||
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
 QY 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
 |||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
 QY 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 8

US-10-466-258-9

; Sequence 9, Application US/10466258
 ; Publication No. US20040132096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GLAXO GROUP LIMITED
 ; TITLE OF INVENTION: ASSAY
 ; FILE REFERENCE: P80966 GCW
 ; CURRENT APPLICATION NUMBER: US/10/466,258
 ; CURRENT FILING DATE: 2003-07-15
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-466-258-9

Query Match 98.1%; Score 5810; DB 16; Length 1192;
 Best Local Similarity 97.2%; Pred. No. 1e-283;
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

QY 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 |||
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 QY 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 |||
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
 QY 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRRG 180
 |||
 Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRRG 180
 QY 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
 |||:|:|

Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQP GNTISAGQEDFPSVLLETAASLP SLSP 240

Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
 |||||

Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy 287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALT KL VKEDEVV 346
 |||||

Db 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALT KL VKEDEVV 360

Qy 347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
 |||||

Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy 407 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
 |||||

Db 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

Qy 467 PLLEDPTSENXTDEKKIEEKKQIVTEKNTSTKTSNPFFVAAQDSETDYVT T DNLT KVTE 526
 ||| |||||

Db 481 PLLGDPTSENKTDEKKIEEKKQIVTEKNTSTKTSNPFLVAAQDSETDYVT T DNLT KVTE 540

Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGT KIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
 |||||

Db 541 EVVANMPEGLTPDLVQEACESELNEVTGT KIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQ P SSSPLEASSVNYESIKHEPENPPPYE 646
 |||||

Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQ P SSSPLEASSVNYESIKHEPENPPPYE 660

Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFS DYSE 705
 |||||

Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFS DYSE 720

Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI 765
 |||||

Db 721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI 780

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
 |||||

Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 826 SNDDLFI SKEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885
 |||||

Db 841 SNDDLFI SKEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS K V L L L P P D V S A L G H 945
 |||||

Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS K V L L L P P D V S A L A - 959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPSTTEKEDRSPSAIF S A D L G K T S V V D L L Y W R D I K K T G V 1005
 ||||| : |

Db 960 TQAEIESIVKPKVLVKEAEKKLPSTTEKEDRSPSAIF S A E L S K T S V V D L L Y W R D I K K T G V 1019

Qy 1006 VFGASL F L L L S L T V F S I V S V T A Y I A L L S V T I S F R I Y K G V I Q A I Q K S D E G H P F R A Y L E S 1065
 |||||

Db 1020 VFGASL F L L L S L T V F S I V S V T A Y I A L L S V T I S F R I Y K G V I Q A I Q K S D E G H P F R A Y L E S 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
 |||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
 |||
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192
 |||

RESULT 9

US-10-408-967-7

; Sequence 7, Application US/10408967
 ; Publication No. US20040063161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn Company
 ; APPLICANT: Yan, Riqiang
 ; APPLICANT: Lu, Yifeng
 ; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
 ; FILE REFERENCE: 00925
 ; CURRENT APPLICATION NUMBER: US/10/408,967
 ; CURRENT FILING DATE: 2003-04-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-967-7

Query Match 97.8%; Score 5794; DB 12; Length 1192;
 Best Local Similarity 97.0%; Pred. No. 6.6e-283;
 Matches 1157; Conservative 4; Mismatches 16; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 |||
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 |||
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP 120
 |||
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP 120
 |||
 Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
 |||
 Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
 |||
 Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
 |||: | : |
 Db 181 SSGSVDETFLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240
 |||
 Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
 |||
 Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300
 |||
 Qy 287 GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV 346
 |||
 Db 301 GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV 360
 |||

Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTIAIYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTIAIYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVM LVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVM LVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLINTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLT VFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLT VFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFPAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 10
 US-09-893-348-18
 ; Sequence 18, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal
 ; APPLICANT: COHEN, Irun R.
 ; APPLICANT: BESERMAN, Pierre
 ; APPLICANT: MOSONEGO, Alon
 ; APPLICANT: MOALEM, Gila
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
 ; FILE REFERENCE: EIS-SCHWARTZ=2A
 ; CURRENT APPLICATION NUMBER: US/09/893,348
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/314,161
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: US 09/218,277
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715
 ; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: IL 124500
 ; PRIOR FILING DATE: 1998-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 1163
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-893-348-18

Query Match 72.5%; Score 4296.5; DB 9; Length 1163;
 Best Local Similarity 74.0%; Pred. No. 1.3e-207;
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

QY 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
 |||:|||| ||||| ||||| ||||| ||||| |||||:||||:|||||
 Db 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEEDDEEEDDEDLEELEVLERK 60
 QY 59 PAAGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118
 ||||| || ||| |||:| :| ||||| |||||: || : |
 Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 QY 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
 ||| ||| ||||| ||||| ||||| || || ||||| |||||
 Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 QY 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
 ||| : |||| |||||:|:||||| |||
 Db 167 RGSGSVDETFLFALPAASEVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
 QY 225 SPLSAAAFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
 |||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
 Db 227 SPLSTVSFKEHGYLGNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286
 QY 285 EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDE 344

Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA---RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTK	523
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQVDPQKQDETVMVLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIQVDPQTEEAVMMLKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDIFSGLAREYTDLEVSHK	882
Db	812	AIYSNDDLLSSKEDKIKESETFSDDSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSA	942
Db	871	SEIANIQSGADSLPCLLPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1107
Qy	1123	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178

Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163

RESULT 11

US-10-267-502-431

; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 431
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431

Query Match 72.2%; Score 4277.5; DB 12; Length 1163;
Best Local Similarity 73.8%; Pred. No. 1.1e-206;
Matches 883; Conservative 108; Mismatches 154; Indels 51; Gaps 19;

QY 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKP 59
|||:||||| ||||| ||||| ||||| |||||:|:||||:|||||
Db 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEDEDEDEDEDEDLEELEVLERKP 60
QY 60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA 119
||||| ||| ||| |||:|| :| ||||| ||||| |||||: || :| |
Db 61 AAGLSAVPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A 114
QY 120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR 179
|| |||| ||||| ||||| || || || || ||||| |||||
Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163
QY 180 GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP SLS 225
|| : ||||| |||||:|:||||| ||||| |||||
Db 164 GSGSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVL FETAASL SLS 223
QY 226 PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE 285
||| |||| ||||| | ||||:| :|||:| :| :||| |||||
Db 224 PLSTVSFKEHGYLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE 283
QY 286 MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALT KLVKEDEV 345
|||||: ||| |||:| | :|||:|:|:|:| :| :| || | |||:|||| |
Db 284 MGSSFN GSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLT KVVKEDGV 342
QY 346 VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404
:| || | ||| :||| |||:||||| |||||: |||: ||| :|||
Db 343 MSPEKTM DIFNEMKMSVVAPVREEYADFKPFEQAW EVKDTYEGSRDVLAA----RANMES 398
QY 405 KVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN 464
|||||| ||||| :| ||||| |||: ||||| :|| | ||||| | :||| | |
Db 399 KVDKKCFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFT-SATESTAA N 457

Qy 465 IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLT KV 524
 Db 458 IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVVAIHDSEADYVTTDNLSKV 516

Qy 525 TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584
 Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP 576

Qy 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPP 643
 Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPP 636

Qy 644 PYEEAMSVSLKVSIGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDY 703
 Db 637 PYEEAMSVALKTSDAKEEIKEPESFNAAAQAEAPYISIACDLIKETKLSTEPSGFSNY 696

Qy 704 SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFES 763
 Db 697 SEIAKFEKSVPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ET 755

Qy 764 MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823
 Db 756 VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA 814

Qy 824 VYSNDDLFIKSEAQIRETETFSDDSSPIEIDEFPTLISSKTD SFSKLAREYTDLEVSHKS 883
 Db 815 IYSNDDLSSKEDKMKESETFSDSSPIEIDEFPTFVSAKDDS----PKEYTDLEVS NKS 870

Qy 884 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SAL 943
 Db 871 EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEF SKSRSSVSKVPLLLPNVSAL 928

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKT 1003
 Db 929 -ESQIEMGNIVKPKVLTKEAEKKLPDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKT 987

Qy 1004 GVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAY 1062
 Db 988 GVVFYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFN 1122
 Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178
 Db 1108 GLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQA KIPGLKRKAE 1163

RESULT 12

US-09-789-386-6

; Sequence 6, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

```

; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6

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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN 240
        |||:|
Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
        -----
Db    186 ----- 185

QY    301 IVANPREEIIIVKNKDEEEKLVSNILHXQQLPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
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Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
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Db    186 ----- 185

QY    421 EKDSSESNDDTSFPTSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTDE 480
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Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL 540
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Db    186 ----- 185

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QY 541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
 Db 186 ----- 185
 QY 601 VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
 Db 186 ----- 185
 QY 661 EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV 720
 Db 186 ----- 185
 QY 721 EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
 Db 186 ----- 185
 QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE 840
 Db 186 ----- 185
 QY 841 TETFSDDSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 Db 186 ----- 185
 QY 901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGHTQAEIESIVKPKVLE 960
 Db 186 ----- 185
 QY 961 KEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
 QY 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
 QY 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335
 QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 13

US-09-765-205-6

; Sequence 6, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6

Query Match 25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLGN 240
          |||:|
Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
          ||
Db    186 ----- 185

QY    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
          ||
Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
          ||
Db    186 ----- 185

QY    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSSENXTDE 480
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Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL 540
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Db    186 ----- 185

QY    541 VQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFESEATPSPVLPDI 600
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Db    186 ----- 185

QY    601 VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
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Db    186 ----- 185
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Qy 661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVDPDHSELV 720
 Db 186 ----- 185
 Qy 721 EDSSPDSEPVDLFSDDSIQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
 Db 186 ----- 185
 Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE 840
 Db 186 ----- 185
 Qy 841 TETFSDDSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 Db 186 ----- 185
 Qy 901 PHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVVSALGHTQAEIESIVKPKVLE 960
 Db 186 ----- 185
 Qy 961 KEAEKKLPDTEKEDRSPSAIFSDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
 Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
 Qy 1081 ALGHVNCTIKELRRLFLVDDLVDLSLFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335
 Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 14

US-09-893-348-24

; Sequence 24, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

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; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
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Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

QY    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPNTISAGQEDFPSVLLETAASXPSLSPLSAA SFKEHEYLGN 240
        |||:|
Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
Db    186 ----- 185

QY    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH 420
Db    186 ----- 185

QY    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDE 480
Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
Db    186 ----- 185

QY    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDI 600
Db    186 ----- 185

QY    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660

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Db 186 ----- 185
 QY 661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV 720
 Db 186 ----- 185
 QY 721 EDSSPDSEPVDFLSDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
 Db 186 ----- 185
 QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840
 Db 186 ----- 185
 QY 841 TETFSOSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 Db 186 ----- 185
 QY 901 PHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLE 960
 Db 186 ----- 185
 QY 961 KEAEKKLPDTEKEDRSPSAIFSAIDLKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVF 1020
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLSLTVF 215
 QY 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
 QY 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFENGLTLLILALISLFSVPVI 1140
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFENGLTLLILALISLFSVPVI 335
 QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 15

US-10-408-967-8

; Sequence 8, Application US/10408967

; Publication No. US20040063161A1

; GENERAL INFORMATION:

; APPLICANT: Pharmacia & Upjohn Company

; APPLICANT: Yan, Riqiang

; APPLICANT: Lu, Yifeng

; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease

; FILE REFERENCE: 00925

; CURRENT APPLICATION NUMBER: US/10/408,967

; CURRENT FILING DATE: 2003-04-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-967-8

Query Match 25.2%; Score 1495.5; DB 12; Length 373;
Best Local Similarity 31.6%; Pred. No. 2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

QY	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
QY	61	AGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
QY	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
QY	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN	240
		:	
Db	181	SSGSV-----	185
QY	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV	300

Db	186	-----	185
QY	301	IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDVVSSSEKAKDSFNEKRV	360

Db	186	-----	185
QY	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH	420

Db	186	-----	185
QY	421	EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDE	480

Db	186	-----	185
QY	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL	540

Db	186	-----	185
QY	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600

Db	186	-----	185
QY	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660

Db	186	-----	185
QY	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720

Db	186	-----	185
QY	721	EDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG	780

Db	186	-----	185

Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKAEQIRE	840
Db	186	-----	185
Qy	841	TETFSOSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	186	-----	185
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	186	-----	185
Qy	961	KEAEKKLPDTEKEDRSPSAIFSAIDLKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	186	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF	215
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	216	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	275
Qy	1081	ALGHVNCTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	276	ALGHVNCTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	335
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	336	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	373

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Job time : 123.281 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:59:39 ; Search time 74.0403 Seconds
(without alignments)
5019.975 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
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16: sp_bacteriaphage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	4851	81.9	986	4	Q8IUA4	Q8iua4 homo sapien
2	4289	72.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
3	4277.5	72.2	1163	11	Q8K3G8	Q8k3g8 mus musculu
4	3658.5	61.8	1046	11	Q8BGK7	Q8bgk7 mus musculu
5	2580.5	43.6	720	11	Q7TNB7	Q7tnb7 mus musculu
6	2527	42.7	639	11	Q8K290	Q8k290 mus musculu
7	2233	37.7	578	11	Q80W95	Q80w95 mus musculu
8	1531	25.8	392	4	Q96B16	Q96b16 homo sapien
9	1201.5	20.3	375	11	Q8BHF5	Q8bhf5 mus musculu
10	1163	19.6	356	11	Q8BH78	Q8bh78 mus musculu
11	1152.5	19.5	357	11	Q8K3G7	Q8k3g7 mus musculu
12	901	15.2	184	6	Q7YRW9	Q7yrw9 bos taurus
13	887	15.0	199	13	Q7T224	Q7t224 gallus gall
14	867	14.6	179	6	Q9GM33	Q9gm33 macaca fasc
15	788.5	13.3	760	13	Q90638	Q90638 gallus gall
16	779	13.2	780	11	Q8K4S4	Q8k4s4 mus musculu
17	778	13.1	780	11	Q8K0T0	Q8k0t0 mus musculu
18	755.5	12.8	214	13	Q7T222	Q7t222 carassius a
19	699	11.8	643	11	Q8CCU2	Q8ccu2 mus musculu
20	688	11.6	199	4	Q9BQ59	Q9bq59 homo sapien
21	672	11.3	208	13	Q90637	Q90637 gallus gall
22	671	11.3	267	11	Q63765	Q63765 rattus sp.
23	626	10.6	237	11	Q8C6D5	Q8c6d5 mus musculu
24	623.5	10.5	236	11	Q8VBU0	Q8vbu0 rattus norv
25	586	9.9	221	13	Q7ZUD6	Q7zud6 brachydanio
26	566	9.6	595	5	Q9VMV9	Q9vmv9 drosophila
27	528	8.9	234	5	Q9VMW3	Q9vmw3 drosophila
28	528	8.9	2484	5	Q9U347	Q9u347 caenorhabdi
29	526	8.9	224	5	Q9VMW1	Q9vmw1 drosophila
30	520	8.8	222	5	Q9VMW4	Q9vmw4 drosophila
31	519.5	8.8	2607	5	Q23187	Q23187 caenorhabdi
32	518	8.7	202	5	Q9VMW2	Q9vmw2 drosophila
33	358.5	6.1	1417	3	Q871Y7	Q871y7 neurospora
34	357.5	6.0	2768	5	Q9VC00	Q9vc00 drosophila
35	343	5.8	107	13	Q7T223	Q7t223 carassius a
36	341.5	5.8	5412	5	Q9W596	Q9w596 drosophila
37	340.5	5.7	222	5	Q23188	Q23188 caenorhabdi
38	339	5.7	1150	5	Q8IMM6	Q8imm6 drosophila
39	334	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila
40	334	5.6	18074	5	Q9I7U4	Q9i7u4 drosophila
41	331	5.6	7962	4	Q10465	Q10465 homo sapien
42	331	5.6	34350	4	Q8WZ42	Q8wz42 homo sapien
43	325.5	5.5	5327	5	O76891	O76891 drosophila
44	322.5	5.4	846	5	Q8MRP6	Q8mrp6 drosophila
45	322.5	5.4	1109	5	Q9VAY4	Q9vay4 drosophila

ALIGNMENTS

RESULT 1

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.

AC Q8IUA4;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE RNT4 (RTN4).
 GN RTN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22376540; PubMed=12488097;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL J. Mol. Biol. 325:299-323(2003).
 DR EMBL; AY102285; AAM64244.1; -.
 DR EMBL; AY123245; AAM64249.1; -.
 DR EMBL; AY123246; AAM64250.1; -.
 DR EMBL; AY123247; AAM64251.1; -.
 DR EMBL; AY123248; AAM64252.1; -.
 DR EMBL; AY123249; AAM64253.1; -.
 DR EMBL; AY123250; AAM64254.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 81.9%; Score 4851; DB 4; Length 986;
 Best Local Similarity 98.9%; Pred. No. 2.4e-231;
 Matches 976; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

Qy	193	MDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTTEGTLQ	252
Db	1	MDLKEQPGNTISAGQEDFPSVLLETAASLPSLSPLSAASFKEHEYLGNLSTVLPTTEGTLQ	60
Qy	253	ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVK	312
Db	61	ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVK	120
Qy	313	NKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD	372
Db	121	NKDEEEKLVSNILHNQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD	180

Qy	373	FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTS	432
Db	181	FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTS	240
Qy	433	FPSTPEGIKDRSGAYITCAPFNPAAATESIATNIFPILLEDPTSENXTDEKKIEEKKQIVT	492
Db	241	FPSTPEGIKDRSGAYITCAPFNPAAATESIATNIFPLLGDPTSENKTDEKKIEEKKQIVT	300
Qy	493	EKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEV	552
Db	301	EKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEV	360
Qy	553	TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDIVMEAPLNSAVPS	612
Db	361	TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDIVMEAPLNSAVPS	420
Qy	613	AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL-KVSGIKEEIKEPENINAA	671
Db	421	AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAA	480
Qy	672	LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVD	731
Db	481	LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVD	540
Qy	732	LFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS	791
Db	541	LFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS	600
Qy	792	LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIE	851
Db	601	LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIE	660
Qy	852	IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP	911
Db	661	IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP	720
Qy	912	KVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSDT	971
Db	721	KVEEKISFSDDFSKNGSATSQVLLLPDVSALA-TQAEIESIVKPKVLVKEAEKKLPSDT	779
Qy	972	EKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL	1031
Db	780	EKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL	839
Qy	1032	ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE	1091
Db	840	ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE	899
Qy	1092	LRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY	1151
Db	900	LRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY	959
Qy	1152	LGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	960	LGLANKNVKDAMAKIQAKIPGLKRKAE	986

08BGM9

Query Match 72.4%; Score 4289; DB 11; Length 1162;
Best Local Similarity 73.9%; Pred. No. 1.7e-203;
Matches 883; Conservative 109; Mismatches 153; Indels 50; Gaps 18;

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Qy      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP 59
      |||:|||| ||||| ||||| |||||:|:|:|:|:|:|:|:|:|
Db      1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEEEEEDEDEDLEELEVLERKP 60

Qy     60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPA 119
      ||||| ||| |||:| | ||||| |||||:| | :|
Db     61 AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A 114

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Qy 120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRR 179
 || ||| ||||| ||||| || || || || ||||| ||||| |||||

Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163

Qy 180 GSSG-----AVVXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP SLS 225
 || : ||||| ||||| : ||||| ||||| ||||| |||||

Db 164 GSGSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLS 223

Qy 226 PLSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE 285
 ||| ||||| ||||| | ||||:| :|||:| :| :||| :||| ||| |||||

Db 224 PLSTVSFKEHGYLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE 283

Qy 286 MGSSFVSVPKAE SAVIVANPREEII VKNKDEEEKLVSNILHXQQELPTALT KLKVEDEV 345
 ||||: ||| |||:| | :||:|:|:|:| : || : || | |||:|||| |

Db 284 MGSSFNGSPKGESAM LVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV 342

Qy 346 VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404
 :| || | ||| :||| ||:|||||||: ||||: | | |:||| :|||

Db 343 MSPEKTM DIFNEMKMSV VAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANMES 398

Qy 405 KVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN 464
 ||||| ||||| | ||||| |:: ||| ||| :|| | ||||| | : :||| | |

Db 399 KVDKKCFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFS-SATESTAAN 457

Qy 465 IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT KV 524
 |||:||| |||| |||||:||||:||| || ||||| || ||| |||||:||

Db 458 IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIH DSEADYVTTDNLSKV 516

Qy 525 TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584
 || ||| ||||| ||||| ||||| |||||:||||| :|||:|| |||||

Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP 576

Qy 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS SSPLEA-SSVNYESIKHEPENPP 643
 ||||:||||| ||||| :|| |||| |||:|||| | |:|: || |||||

Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPP 636

Qy 644 PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFSDY 703
 |||||:||| | |||||: ||| ||| ||||| ||||| |||:|:|:|

Db 637 PYEEAMSVALKTSDSKEEIKEPESFNAAAQEA EAPYIS IACDLIKETKLSTEPSPEFSNY 696

Qy 704 SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFES 763
 ||:|| |: |||| |||:||||:||||| ||||:|| |:| |||:|||| | |:

Db 697 SEIAKFEKSVPDHC ELVDDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL TEVS-ET 755

Qy 764 MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823
 : :||:|:| ||| | |||||: |: ||| :||: ||| | ||||| :||

Db 756 VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLT KKETISLQMEEFNTA 814

Qy 824 VYSNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKS 883
 :||| ||| :||:| ||||| ||||| :|| || :|||:|:|

Db 815 IYSNDDLSSKEDKMKESETFSDSSPIEII DEFPTFVSAKDDS----PKEYTDLEVS NKS 870

Qy 884 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATSKVLLLPPDV SAL 943
 |||| | ||||:||| ||| || | : ||:||| |: ||| || |:|||

Db 871 EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEF SKSRSSSVSKVPLLLPNVSAL 928

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKT 1003

Db	929	-ESQIEMGNIVKPKVLTKEAEELPSDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKT	987
Qy	1004	GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYL	1063
Db	988	GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYL	1047
Qy	1064	ESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNG	1123
Db	1048	ESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNG	1107
Qy	1124	LTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1108	LTLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE	1162

Q8K3G8

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ID      Q8K3G8                PRELIMINARY;          PRT;  1163 AA.
AC      Q8K3G8;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nogo-A.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Jin W., Long M., Li R., Ju G.;
RT      "Cloning and expression of the mouse Nogo-A protein.";
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY114152; AAM77068.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;

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Query Match 72.2%; Score 4277.5; DB 11; Length 1163;
Best Local Similarity 73.8%; Pred. No. 6.2e-203;
Matches 883; Conservative 108; Mismatches 154; Indels 51; Gaps 19;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		: : : :	
Db	1	MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		: : : :	
Db	61	AAGLSAVPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPAPAPAAPSTPAAPKRR	179

Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS	225
Db	164	GSGSVDETLFALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLS	223
Qy	226	PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE	285
Db	224	PLSTVSFKEHGYLGNLSAVASTEGETIETLNEASRELPERATNPFVNRESAEFSVLEYSE	283
Qy	286	MGSSFSVSPKAESAVIVANPREELIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEV	345
Db	284	MGSSFNKSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV	342
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES	404
Db	343	MSPEKTMDIFNEMKMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDLVLA-----RANMES	398
Qy	405	KVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN	464
Db	399	KVDKKCFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFT-SATESTAAN	457
Qy	465	IFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKV	524
Db	458	IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVLVAIHDEADYVTTDNLISKV	516
Qy	525	TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCP	584
Db	517	TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSSEAIQESIYPTAQLCP	576
Qy	585	SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENPP	643
Db	577	SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPP	636
Qy	644	PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDY	703
Db	637	PYEEAMSVALKTSDAKEEIKEPESFNAAAQAEAPYISIIACDLIKETKLSTEPSPGFSNY	696
Qy	704	SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFES	763
Db	697	SEIAKFEKSVDPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ET	755
Qy	764	MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA	823
Db	756	VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA	814
Qy	824	VYSNDDLFIKSEAQIRETETFSDDSPIEIIIDEFPTLISSKTDSDFSKLAREYTDLEVSHKS	883
Db	815	IYSNDDLSSKEDKMKESSETFSDDSPIEIIIDEFPTFVSAKDDS----PKEYTDLEVSNKS	870
Qy	884	EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA	943
Db	871	EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFSKSRSSSVSKVPLLLPNVSAL	928
Qy	944	GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKT	1003

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Db          929 -ESQIEMGNIVKPKVLTKEAEEKLPSDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKT 987
QY          1004 GVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1062
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          988 GVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1047
QY          1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1122
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107
QY          1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
            |||||||||||||||:|||||||||||||||||:|||||||||||||||||
Db          1108 GLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1163

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RESULT 4

Q8BGK7

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ID   Q8BGK7          PRELIMINARY;          PRT; 1046 AA.
AC   Q8BGK7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102280; AAM73502.1; -.
DR   EMBL; AY102286; AAM73507.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.

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DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 61.8%; Score 3658.5; DB 11; Length 1046;

Best Local Similarity 69.5%; Pred. No. 2e-172;

Matches 767; Conservative 108; Mismatches 148; Indels 81; Gaps 17;

```
Qy      97 APPVAPERQ-----PSWDPS-----PVSSTVPAP---SPLSAAAVSPSKLPED 136
      |||:| | :| || | || | | |||
Db      2 APPLAGGGQKGGAASEAWVPSLFGVSGSTCTAAKSLVPIPARSSRLSAA----- 51

Qy     137 DEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLK 196
      : | :: || | : | | :: : |||||
Db      52 -----RNETLFALPA---ASEPVIPSSAE-----KIMDLK 78

Qy     197 EQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGNLSTVLPTEGTLQENV 256
      |||||:|:||||||| ||||| ||||| ||||| ||||| | ||||:| :|
Db      79 EQPGNTVSSGQEDFPSVLFFETAASLPSLSPLSTVSFKEHGYLGNLSAVASTEGTIEETLN 138

Qy     257 EASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVKNKDE 316
      |||:|: | :| :|: || ||| ||||| |||||: ||| |||:| | :||:|:|:|:|
Db     139 EASRELPERATNPFVNRESAEFSVLEYSEMGSFNGSPKGESAMLVENTKEEVIVRSKDK 198

Qy     317 EEKLVSNNILHXQQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376
      |: || : || || | |||:|||| |:| || | ||| :::| |:| ||||| |||||
Db     199 ED-LVCSAALHNPQESPATLTQVVKEDGVMSPEKTMDFNEMKMSVVAPVREEYADFKPF 257

Qy     377 ERVWEVKDSKEDS-DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPS 435
      |: |||||: | | |:||| :|:||||||| ||||| | ||||| |:| |||
Db     258 EQAWEVKDITYEGSRDVLAA----RANMESKVDKKCFEDSLEQKGHGKDSSESRNENASFFR 313

Qy     436 TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKN 495
      ||| :|| | |||| |: :||| | |||:|| ||| |||||:||||:|
Db     314 TPELVKDGSRAYITCDSFS-SATESTAANIFFVLEDHTSENKTDEKKIEERKAQIITEK- 371

Qy     496 TSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEVTGT 555
      || ||||| || |||||:|||| || ||||| ||||| ||||| ||||| |||||
Db     372 TSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACESELNEATGT 431

Qy     556 KIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGA 615
      |||||:| ||||| :||:| |||||:| ||||| ||||| ||||| :|| ||
Db     432 KIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGA 491

Qy     616 SVIQPSSSPLEA-SSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAALQE 674
      || |||:|||| | |:|: || ||||| |||||:| | |||||: ||| ||
Db     492 SVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQE 551

Qy     675 TEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS 734
      ||||| ||||| ||||| |||:|:|:|:|:| |: |||| |||:|:|:|:|:|
Db     552 AEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVDPDHCELVDSSPESEPVDLFS 611

Qy     735 DDSIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDN 794
      |||||:| ||| |||:|||| | |:| :::|:|:| || | |||||: |
Db     612 DDSIPEVPQTQEEAVMLMKESLTEVS-ETVTQHKHKERLSASPQEVGKPYLESFQPNLHI 670

Qy     795 TKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDDSPIEIID 854
      ||| :|: ||:| || ||||| :|:| ||||| ||| :::|:| ||||| |||||
```

Db 671 TKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDLSSKEDKMKESETFSDSSPIEIID 729

Qy 855 EFPTLISSKTDSEFSKLAAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE 914
 |||| :|:| || :|||||||:||||| || ||||:|| || || || ||

Db 730 EFPTFVSAKDDSD---PKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE 785

Qy 915 EKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPDTEKE 974
 : ||:||||: |: ||| || |:|||| :| |: :|||||| ||||:|||||||

Db 786 AHV--SDEFSKSRSSSVSKVPLLLPNVSAL-ESQIEMGNIVKPKVLTKEAEKLPDTEKE 842

Qy 975 DRSPSAIFSAADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034
 ||| :|: ||:| |||||||||||||||||||||||||||||||||||||||

Db 843 DRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 902

Qy 1035 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094
 ||||||||||||||||||||||||||||||||||||||| |||||

Db 903 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 962

Qy 1095 LFLVDDLVDLTKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154
 ||||||||||||||||||||||||||||||||||||||:|||||||||

Db 963 LFLVDDLVDLTKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 1022

Qy 1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||:|||||||||||||||||

Db 1023 ANKSVKDAMAKIQAKIPGLKRKAE 1046

RESULT 5

Q7TNB7

ID Q7TNB7 PRELIMINARY; PRT; 720 AA.

AC Q7TNB7;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC056373; AAH56373.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;

Query Match 43.6%; Score 2580.5; DB 11; Length 720;
 Best Local Similarity 70.8%; Pred. No. 2.1e-119;
 Matches 527; Conservative 69; Mismatches 107; Indels 41; Gaps 13;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		: : : : : : : : : :	
Db	1	MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		: : :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP SLS	225
		: : : : : :	
Db	164	GGSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFE TAASLPSLS	223
Qy	226	PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE	285
		: : : : : : : :	
Db	224	PLSTVSFKEHGYLGNLSAVASTEGTIEETLINEASRELPERATNPFVNRESAEFSVLEYSE	283
Qy	286	MGSSFSVSPKAESAVIVANPREELIVKNKDDEEKLVSNNILHXQQELPTALTCLKVKEDEV	345
		: : : : : : : : : :	
Db	284	MGSSFNGSPKGESAMLVNTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV	342
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES	404
		: : : : : : : : :	
Db	343	MSPEKTMDIFNEMKMSV VAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANMES	398
Qy	405	KVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN	464
		: : : :	
Db	399	KVDKKCFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFS-SATESTAAN	457
Qy	465	IFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT KV	524
		: : : :	
Db	458	IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIH DSEADYVTTDNLSKV	516
Qy	525	TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKM DLVQTSEVMQESLYPAAQLCP	584
		: : : :	

Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP 576

QY 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPP 643
 ||||:||||||||||||||||||:| |||| |||:|||| | |:|: || |||||

Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPP 636

QY 644 PYEEAMSVSLKVGSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDY 703
 |||||:|| | |||||: ||| || ||||| ||||| |||:|:|:|

Db 637 PYEEAMSVALKTSDSKEEIKEPESFNAAAQAEAPYISIACDLIKETKLSTEPSPEFSNY 696

QY 704 SEMAKVEQVPDPHSELVEDSSPDS 727
 ||:| | |: ||| |||:||||:|

Db 697 SEIAKFEKSVPDPHCELVDDSSPES 720

RESULT 6

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.

AC Q8K290;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC032192; AAH32192.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

KW Hypothetical protein.

SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 42.7%; Score 2527; DB 11; Length 639;

Best Local Similarity 79.5%; Pred. No. 7.7e-117;

Matches 515; Conservative 57; Mismatches 66; Indels 10; Gaps 6;

Qy 532 MPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEA 591
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEA 60

Qy 592 TPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPPPYEEAMS 650
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 TPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMS 120

Qy 651 VSLKVGSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVE 710
 |:| | |||||: ||| || ||||| ||||| ||||| ||||| ||||| |||||

Db 121 VALKTSDAKEEIKEPESFNAAAQAEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFE 180

FT NON_TER 1 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 37.7%; Score 2233; DB 11; Length 578;
Best Local Similarity 78.4%; Pred. No. 2.2e-102;
Matches 460; Conservative 52; Mismatches 65; Indels 10; Gaps 6;

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Qy      593 PSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEA-SSVNYESIKHEPENPPPPYEEAMSV 651
          ||||| :|| ||| ||:|||| | |:| || |||||
Db      1 PSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPPYEEAMSV 60

Qy      652 SLKVSIGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQ 711
          :|| | |||||: ||| || ||||| ||||| ||:| ||:||||:| | :
Db      61 ALKTSDAKEEIKEPESFNAAAQEAEPYISIIACDLIKETKLSTEPSPGFSNYSEIAKFEK 120

Qy      712 PVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKE 771
          ||| |||:||||:|||||:|||| |:| |||:|||| | |:| ::::|
Db      121 SVPDHCELVDDSSPESEFPVDFSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVTQHKHKE 179

Qy      772 KLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLF 831
          :||| | |||||: :| ||| :| ||| | |||| :||:|||||
Db      180 RLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDLL 238

Qy      832 ISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDG 891
          ||| ::|:|||||:||||| :|:| || :|||||:||||| |
Db      239 SSKEDKMKESETFSDDSPIEIIDEFPTFVSAKDDS---PKEYTDLEVSNNKSEIANVQSG 294

Qy      892 AGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLLPPDVSA LGHTQAEIE 951
          | ||||:|||| ||| || | | : ||:|||| |: | || || |:|||| :| |:
Db      295 ANSLPCSELPCDLSFKNTYPKDEAHV--SDEFSSKRSVFKVPLLLPNVSAL-ESQIEMG 351

Qy      952 SIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL 1011
          :||||| ||||:|||||:||||| :|: ||:| ||||| |||||
Db      352 NIVKPKVLTKEAEKKLPDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASL 411

Qy      1012 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      412 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 471

Qy      1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 1131
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      472 ELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 531

Qy      1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||||:||||| |||||:||||| ||||| ||||| ||||| |||||
Db      532 ISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 578
```

RESULT 8

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (RTN4).
GN RTN4.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22376540; PubMed=12488097;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL J. Mol. Biol. 325:299-323(2003).
 DR EMBL; BC016165; AAH16165.1; -.
 DR EMBL; AY102285; AAM64242.1; -.
 DR EMBL; AY102278; AAM64247.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 25.8%; Score 1531; DB 4; Length 392;
 Best Local Similarity 32.4%; Pred. No. 6.1e-68;
 Matches 382; Conservative 7; Mismatches 3; Indels 786; Gaps 4;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
 Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
 Qy 181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN 240

Db	181	SSGSV-----	185
Qy	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV	300
Db	186	-----	185
Qy	301	IVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV	360
Db	186	-----	185
Qy	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH	420
Db	186	-----	185
Qy	421	EKDSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTDE	480
Db	186	-----DETLE-----	190
Qy	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL	540
Db	191	-----	190
Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	191	-----	190
Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	191	-----ALPAA-----	195
Qy	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	196	-----	195
Qy	721	EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Db	196	-----SEPV-----	199
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE	840
Db	200	-----	199
Qy	841	TETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	200	-----	199
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	200	-----	199
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSAIDLKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	200	-----IRSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	234
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080

Db 235 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 294

QY 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
 |||

Db 295 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 354

QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||

Db 355 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392

RESULT 9

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.

AC Q8BHF5;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7;

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=129SvcJ7;

RA Van der Putten H., Mir A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY102282; AAM73504.1; -.

DR EMBL; AY102286; AAM73509.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match

20.3%; Score 1201.5; DB 11; Length 375;

Best Local Similarity 28.6%; Pred. No. 1.1e-51;
Matches 337; Conservative 17; Mismatches 20; Indels 805; Gaps 11;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
Db	1	MEDIDQSSSLVSSSADSPRPPPAFKYQFVTEPEDEEDEDEDEDEDEDEDELEELVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPA	119
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS--A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLKVEDVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTD	479
Db	166	-----GSVDETLF-----	173
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD	539
Db	174	-----	173
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPD	599
Db	174	-----	173
Qy	600	IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK	659
Db	174	-----ALPAA-----	178
Qy	660	EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL	719
Db	179	-----	178
Qy	720	VEDSSPDSEPVDLFSDDSIQDPVQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE	779
Db	179	-----SEPV-----	182
Qy	780	GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKESQAQIR	839

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Db      183 ----- 182
Qy      840 ETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899
Db      183 ----- 182
Qy      900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVVSALGHTQAEIESIVKPKVL 959
Db      183 ----- 182
Qy      960 EKEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTV 1019
          :||                               ::|||
Db      183 -----IPS-----SAVVDLLYWRDIKKTGVVFGASLFLLLSLTV 216
Qy      1020 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSN 1079
          |||
Db      217 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSN 276
Qy      1080 SALGHVNCTIKELRRLFLVDDLVDSLKFVAVLMWVFTYVGALENGLTLLILALISLFSVPV 1139
          |||
Db      277 SALGHVNSTIKELRRLFLVDDLVDSLKFVAVLMWVFTYVGALENGLTLLILALISLFSIPV 336
Qy      1140 IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||
Db      337 IYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 375

```

RESULT 10

Q8BH78

```

ID   Q8BH78          PRELIMINARY;      PRT;   356 AA.
AC   Q8BH78;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

```

RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102281; AAM73503.1; -.
 DR EMBL; AY102286; AAM73508.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 19.6%; Score 1163; DB 11; Length 356;
 Best Local Similarity 27.7%; Pred. No. 8e-50;
 Matches 326; Conservative 12; Mismatches 17; Indels 824; Gaps 8;

Qy	1	MEDLDQSPVLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		: : : :	
Db	1	MEDIDQSSVLVSSSADSPRPPLPAFKYQFVTEPEDEEDEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		: : :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS--A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPFAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPD	599

Db 166 ----- 165
 Qy 600 IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVS GIK 659
 Db 166 ----- 165
 Qy 660 EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSEL 719
 Db 166 ----- 165
 Qy 720 VEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPE 779
 Db 166 ----- 165
 Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIR 839
 Db 166 ----- 165
 Qy 840 ETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899
 Db 166 ----- 168
 Qy 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLLPPDV SALGHTQAEIESIVKPKVL 959
 Db 169 ----- 168
 Qy 960 EKEAEKKLP SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASL FLLLSLTV 1019
 Db 169 ----- 197
 Qy 1020 FSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSN 1079
 Db 198 FSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSN 257
 Qy 1080 SALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPV 1139
 Db 258 SALGHVNSTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPV 317
 Qy 1140 IYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178
 Db 318 IYERHQAQIDHYLGLANKSVKDAMAKIQA KIPGLKRKAE 356

RESULT 11

Q8K3G7

ID Q8K3G7 PRELIMINARY; PRT; 357 AA.

AC Q8K3G7;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nogo-B.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jin W., Li R., Long M., Shen J., Ju G.;
 RT "Cloning and expression of the mouse Nogo-B protein."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY114153; AAM77069.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 19.5%; Score 1152.5; DB 11; Length 357;
 Best Local Similarity 27.6%; Pred. No. 2.6e-49;
 Matches 326; Conservative 12; Mismatches 17; Indels 825; Gaps 9;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		: : : :	
Db	1	MEDIDQSSSLVSSSADSPPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		: : : :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTFPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSPFEESEATPSPVLPD	599
Db	166	-----	165

Qy 600 IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK 659

Db 166 ----- 165

Qy 660 EEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSEL 719

Db 166 ----- 165

Qy 720 VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE 779

Db 166 ----- 165

Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIR 839

Db 166 ----- 165

Qy 840 ETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899

Db 166 ----- ||: GSV---- 168

Qy 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVVSALGHTQAEIESIVKPKVL 959

Db 169 ----- 168

Qy 960 EKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLT 1018

Db 169 ----- ||||| ||||| VVDLLYWRDIKKTGVVYFGASLFLLLSLT 197

Qy 1019 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 1078

Db 198 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 257

Qy 1079 NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP 1138

Db 258 NSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 317

Qy 1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

Db 318 VIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 357

RESULT 12

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.

AC Q7YRW9;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4w (Fragment).

GN RTN4.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; AAP47319.1; -.
FT NON_TER 1 1
SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

Query Match 15.2%; Score 901; DB 6; Length 184;
Best Local Similarity 98.9%; Pred. No. 2.8e-37;
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 995 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 1054
|||||
Db 1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 60
Qy 1055 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 1114
|||||
Db 61 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 120
Qy 1115 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 1174
|||||
Db 121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180
Qy 1175 RKAE 1178
||||
Db 181 RKAE 184

RESULT 13

Q7T224

ID Q7T224 PRELIMINARY; PRT; 199 AA.
AC Q7T224;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4-C.
GN RTN4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164737; AAP47312.1; -.
SQ SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 15.0%; Score 887; DB 13; Length 199;
Best Local Similarity 88.2%; Pred. No. 1.6e-36;

Matches 180; Conservative 7; Mismatches 11; Indels 6; Gaps 1;

```
Qy      975 DRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034
      |  ||      |  |||||||||||||||||||||||||||||||||||||||
Db      2 DSQPSG-----WKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 55

Qy     1035 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094
      |||||||||||||||||||||||||||||||:|:|:|:|:|:|:|:|:|:|:|:|
Db      56 SVTISFRIYKGVIAIQKSDEGHPFRAYLES DVAVSED LIQKYSSVLGHINGTVKELRR 115

Qy     1095 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     116 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 175

Qy     1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178
      |||||||||||||||||||
Db     176 VNKNVKDAMAKIQAKIPGLKRKTE 199
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RESULT 14

Q9GM33

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ID   Q9GM33      PRELIMINARY;      PRT;   179 AA.
AC   Q9GM33;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049853; BAB16739.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;
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Query Match 14.6%; Score 867; DB 6; Length 179;
Best Local Similarity 98.3%; Pred. No. 1.3e-35;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1000 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPF 1059
      :|||||||||||||||||||||||||||||:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRQVIAIQKSDEGHPF 60

Qy     1060 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 1119
```

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      |||||||:|||||
Db      61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLRFVLMWVFTYVGA 120

Qy      1120 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
      |||||||
Db      121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

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RESULT 15

Q90638

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ID      Q90638      PRELIMINARY;      PRT;      760 AA.
AC      Q90638;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      ChS-Rex-b (RTN1-A).
GN      RTN1.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=96386034; PubMed=8793864;
RA      Baka I.D., Ninkina N.N., Pinon L.G., Adu J., Davies A.M.,
RA      Georgiev G.P., Buchman V.L.;
RT      "Intracellular compartmentalization of two differentially spliced s-
RT      rex/NSP mRNAs in neurons.";
RL      Mol. Cell. Neurosci. 7:289-303(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=97183663;
RA      Ninkina N.N., Baka I.D., Buchman V.L.;
RT      "Rat and chicken s-rex/NSP mRNA: nucleotide sequence of main
RT      transcripts and expression of splice variants in rat tissues.";
RL      Gene 184:205-210(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; U17606; AAC60075.1; -.
DR      EMBL; AY164724; AAP47301.1; -.
DR      GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      760 AA; 82502 MW; 465C1B429F799D5C CRC64;

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Query Match      13.3%; Score 788.5; DB 13; Length 760;
Best Local Similarity 27.7%; Pred. No. 7e-31;
Matches 296; Conservative 115; Mismatches 315; Indels 341; Gaps 38;

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Qy 143 PPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNT 202
 || | : | | | | | | : |
 Db 4 PPDPQDLLLAGTAER-W-----AAAGADEYAAGAALRDGDGA-----QOREQL 45

 Qy 203 ISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEV 262
 : | | : || | | : : | | : | : : |
 Db 46 AFGSAREHPPVAMATA-----SPGVTASSRLFDY-----GSSSANGADSSFYT 88

 Qy 263 SEKAKTLLID-----RDLTEFSELEYSEMSSFSVSPKAESAVIVANPREEIIVKNKDE 316
 | : | | | : : | : | | : : | : : |
 Db 89 S-----LISDVHYTTPRDNTYFTGV-YQQENSPIPCSTEGFNALGHPVQDV---TGFE 139

 Qy 317 EEKLVSNILHXQQELPTALTCLKVEDEVSSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376
 | | | : : | | | : : | : | :
 Db 140 SRGLFS-----LDSGIEMTPAESAE-----EVDKSLTDPMKVEGYKYMDI 178

 Qy 377 ERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSSESSNDD--TSFP 434
 | : | | | : | : | : | :
 Db 179 SRPEEIK-----YQEKHDPDSEDESPDLIDEYR 206

 Qy 435 STPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKQIVTEK 494
 || | | : : | | : | | : : | : | :
 Db 207 GTPIG---SGH--AAEPQRTTASEAIIKA---PKEQDPLE---DKSFRDQHNASVVTAP 253

 Qy 495 NTSTKTSNPFVAAQDSETDYVTTDNLTKEVEEVVANM---PE-----GLTP 538
 | | | | : : | : | : | : | :
 Db 254 VKITLTETPGAREATSKEASVTQPKSGLKPSHEVVPTVMVSEPDDSPGSVTPPSSGTEP 313

 Qy 539 DLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFEESEATPSPVLP 598
 : : | : | | : | : | : | : | : | :
 Db 314 SGSESQKGKSLSEDELISAIKEAKGFSFETSEVQQS---PAV---SAEKQEQKMKPGRP 366

 Qy 599 DIVMEAPLNSAVPSA--GASVIQ-PSSSPLEASSV---NYESIKHEPENPPPYEEAMSVS 652
 : : | : : | | | : | | | | : | : | : | :
 Db 367 --AVPSPLDNEASSAESGDSEIELVSEDPLAAEEVLHSNYMTFSH-IGGPPP--SPASPS 421

 Qy 653 LKVSGIKKEEIKPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQP 712
 : : | : : | : : | : | : : | : | : | :
 Db 422 IQYSILREERE-----AELDSELIIESCD---ASSASEESP-----KREQD 459

 Qy 713 VPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLESILTETSFESMIEYENKEK 772
 | : | | : : | : | : | : | :
 Db 460 SPLMKPMVMD-----IIEK-----ENSSR 478

 Qy 773 LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI 832
 || | |
 Db 479 ASASDYE----- 485

 Qy 833 SKEAQIRETETTFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA 892
 : | | | : : | : | : | : | :
 Db 486 -----ASKTTE-SRMNRE-----NLADSA 503

 Qy 893 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIES 952
 | : : | : | : | : : : :
 Db 504 SYLKSS-----FVAPKVSSE-----PPTSASVSTEELKERI 533

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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:58:54 ; Search time 15.6624 Seconds
(without alignments)
3916.307 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPILVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
		Query					
Result	No.	Score	Match	Length	DB	ID	Description
1	5815	98.2	1192	1	RTN4_HUMAN	Q9nqc3	homo sapien
2	4296.5	72.5	1163	1	RTN4_RAT	Q9jkl1	rattus norv
3	915	15.4	199	1	RTN4_MOUSE	Q99p72	mus musculu
4	791	13.4	777	1	RTN1_RAT	Q64548	rattus norv
5	787.5	13.3	776	1	RTN1_HUMAN	Q16799	homo sapien
6	626	10.6	237	1	RTN3_MOUSE	Q9es97	mus musculu
7	625.5	10.6	236	1	RTN3_HUMAN	O95197	homo sapien
8	514	8.7	545	1	RTN2_HUMAN	O75298	homo sapien
9	500	8.4	471	1	RTN2_MOUSE	O70622	mus musculu
10	324.5	5.5	865	1	CPN_DROME	Q02910	drosophila
11	320	5.4	5147	1	PCLO_HUMAN	Q9y6v0	homo sapien
12	315	5.3	5038	1	PCLO_MOUSE	Q9qyx7	mus musculu
13	299	5.0	3924	1	ANK2_HUMAN	Q01484	homo sapien
14	296.5	5.0	2468	1	MAPB_HUMAN	P46821	homo sapien
15	289	4.9	2459	1	MAPB_RAT	P15205	rattus norv
16	289	4.9	2464	1	MAPB_MOUSE	P14873	mus musculu
17	287	4.8	5120	1	PCLO_CHICK	Q9pu36	gallus gall

18	286.5	4.8	3644	1	MINT_MOUSE	Q62504	mus musculu
19	276	4.7	5085	1	PCLO_RAT	Q9jks6	rattus norv
20	273.5	4.6	3664	1	MINT_HUMAN	Q96t58	homo sapien
21	264.5	4.5	8545	1	ANCL1_CAEEL	Q9n4m4	caenorhabdi
22	263.5	4.4	3396	1	PGCV_HUMAN	P13611	homo sapien
23	262.5	4.4	6632	1	UN89_CAEEL	O01761	caenorhabdi
24	260.5	4.4	3381	1	PGCV_BOVIN	P81282	bos taurus
25	259.5	4.4	1828	1	MAP2_MOUSE	P20357	mus musculu
26	258.5	4.4	2805	1	MAPA_HUMAN	P78559	homo sapien
27	258	4.4	1616	1	P200_MYCGE	Q49429	mycoplasma
28	257.5	4.3	1781	1	AK12_HUMAN	Q02952	homo sapien
29	257.5	4.3	2738	1	PGCV_RAT	Q9erb4	rattus norv
30	253	4.3	1189	1	YJH6_YEAST	P47035	saccharomyc
31	252	4.3	4377	1	ANK3_HUMAN	Q12955	homo sapien
32	250.5	4.2	1861	1	MAP2_RAT	P15146	rattus norv
33	249.5	4.2	1827	1	MAP2_HUMAN	P11137	homo sapien
34	248	4.2	3421	1	TEGU_HSVEB	P28955	equine herp
35	244	4.1	1362	1	BRD4_HUMAN	O60885	homo sapien
36	242	4.1	1790	1	USO1_YEAST	P25386	saccharomyc
37	239	4.0	1744	1	TANA_XENLA	Q01550	xenopus lae
38	238.5	4.0	1411	1	TCOF_HUMAN	Q13428	homo sapien
39	236.5	4.0	3358	1	PGCV_MOUSE	Q62059	mus musculu
40	235.5	4.0	1723	1	AIM1_HUMAN	Q9y4k1	homo sapien
41	233.5	3.9	1087	1	NFH_MOUSE	P19246	mus musculu
42	232	3.9	1140	1	YM96_YEAST	Q04893	saccharomyc
43	231	3.9	3256	1	KI67_HUMAN	P46013	homo sapien
44	229.5	3.9	1367	1	AMYPH_YEAST	P08640	saccharomyc
45	228.5	3.9	1306	1	MSB2_YEAST	P32334	saccharomyc

ALIGNMENTS

RESULT 1

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN RTN4 OR NOGO OR ASY OR KIAA0886.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans."
RL Nature 403:383-384(2000).
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21010696; PubMed=11126360;
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
 RL Oncogene 19:5736-5746(2000).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20237542; PubMed=10773680;
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
 RT 2p14-->2p13 by radiation hybrid mapping.";
 RL Cytogenet. Cell Genet. 88:101-102(2000).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 4).
 RA Jin W.-L., Ju G.;
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Placenta, and Skeletal muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742;
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.

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 CC -----

DR EMBL; AJ251383; CAB99248.1; -.
 DR EMBL; AJ251384; CAB99249.1; -.
 DR EMBL; AJ251385; CAB99250.1; -.
 DR EMBL; AB040462; BAB18927.1; -.
 DR EMBL; AB040463; BAB18928.1; -.
 DR EMBL; AF148537; AAG12176.1; -.
 DR EMBL; AF148538; AAG12177.1; -.
 DR EMBL; AF087901; AAG12205.1; -.
 DR EMBL; AF320999; AAG40878.1; -.
 DR EMBL; AF132047; AAD31021.1; -.
 DR EMBL; AF132048; AAD31022.1; -.

DR EMBL; AB015639; BAA83712.1; -.
DR EMBL; AF077050; AAD27783.1; -.
DR EMBL; AF177332; AAG17976.1; -.
DR EMBL; AB020693; BAA74909.1; -.
DR EMBL; BC001035; AAH01035.1; -.
DR EMBL; BC007109; AAH07109.1; -.
DR EMBL; BC014366; AAH14366.1; -.

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSP	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSP	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKPENINAALOETEAPYISIIACDLIKETKLSAEPAPDFS DYSE	705

RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20129258; PubMed=10667796;
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A.A., Christ F., Schwab M.E.;
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1.";
 RL Nature 403:434-439(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=22033691; PubMed=12037567;
 RA GrandPre T., Li S., Strittmatter S.M.;
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
 RL Nature 417:547-551(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----

DR EMBL; AF051335; AAF01564.1; -.
 DR EMBL; AJ242961; CAB71027.1; -.
 DR EMBL; AJ242962; CAB71028.1; -.
 DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).
 FT TRANSMEM 990 1010 POTENTIAL.
 FT DOMAIN 1011 1104 LUMENAL (Potential).
 FT TRANSMEM 1105 1125 POTENTIAL.
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).
 FT DOMAIN 976 1163 RETICULON.
 FT DOMAIN 33 46 POLY-GLU.
 FT DOMAIN 73 76 POLY-ALA.
 FT DOMAIN 140 145 POLY-PRO.
 FT VARSPLIC 1 964 Missing (in isoform 3).
 FT /FTId=VSP_005656.
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).
 FT /FTId=VSP_005657.
 FT VARSPLIC 173 975 Missing (in isoform 2).
 FT /FTId=VSP_005658.
 FT VARSPLIC 192 975 Missing (in isoform 4).
 FT /FTId=VSP_005659.
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 72.5%; Score 4296.5; DB 1; Length 1163;
 Best Local Similarity 74.0%; Pred. No. 2e-157;
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
 |||:|||| ||||| ||||| ||||| ||||| |||||:|:|||||||
 Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEDDEEDEDLEELEVLERK 60
 Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118
 ||||| || ||| |||:|:| ||||| |||||: || : |
 Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA--P 115
 Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
 ||| |||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
 ||| : ||||| |||||:|:||||||| |||
 Db 167 RGSGSVDETFLFALPAASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
 Qy 225 SPLSAAAFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284

Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKKAIQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLT	523
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPPFLVAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIQEVQQTQEEAVMLKESLTVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESSETFSDDSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVS	942
Db	871	SEIANIQSGADSLPCLLPCLDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMVFTYVGALFN	1122

Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||||:||||| |||||:|||||

Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 3

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).

GN RTN4 OR NOGO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3T3-L1; TISSUE=Adipocyte;

RA Coulson A.C., Craggs P.D., Morris N.J.;

RT "Mouse vp20/RTN4C cDNA.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 170-199 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults (By

CC similarity).

CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By

CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the

CC membrane of the endoplasmic reticulum through 2 putative

```

transmembrane domains (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=1;
CC          Comment=A number of isoforms may be produced;
CC          Name=1;
CC          IsoId=Q99P72-1; Sequence=Displayed;
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF326337; AAK08076.1; -.
DR      EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR      GO; GO:0005635; C:nuclear membrane; ISS.
DR      GO; GO:0005515; F:protein binding; ISS.
DR      GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR      GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN      1      25      CYTOPLASMIC (Potential).
FT      TRANSMEM      26      50      POTENTIAL.
FT      DOMAIN      51      137      LUMENAL (Potential).
FT      TRANSMEM      138      162      POTENTIAL.
FT      DOMAIN      163      199      CYTOPLASMIC (Potential).
FT      DOMAIN      12      199      RETICULON.
SQ      SEQUENCE      199 AA;  22466 MW;  07BE5D580059ED9C CRC64;

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RESULT 4

RTN1_RAT

ID RTN1_RAT STANDARD; PRT; 777 AA.
AC Q64548; Q64547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN RTN1 OR NSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC STRAIN=Wistar; TISSUE=Brain cortex;
RX MEDLINE=96386034; PubMed=8793864;
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA Georgiev G.P., Buchman V.L.;
RT "Intracellular compartmentalization of two differentially spliced s-
RT rex/NSP mRNAs in neurons."
RL Mol. Cell. Neurosci. 7:289-303(1996).
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC membrane trafficking in neuroendocrine cells.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RTN1-B; Synonyms=S-RexB;
CC IsoId=Q64548-1; Sequence=Displayed;
CC Name=RTN1-S; Synonyms=S-RexS;
CC IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC TYPES.
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC HINDBRAIN.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; U17604; AAC53046.1; -.
DR EMBL; U17603; AAC53045.1; -.

DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 604 624 POTENTIAL.
 FT TRANSMEM 727 747 POTENTIAL.
 FT DOMAIN 590 777 RETICULON.
 FT DOMAIN 610 613 POLY-LEU.
 FT VARSPLIC 1 569 Missing (in isoform RTN1-S).
 FT /FTid=VSP_005647.
 FT VARSPLIC 570 589 IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-S).
 FT /FTid=VSP_005648.
 SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

Query Match 13.4%; Score 791; DB 1; Length 777;
 Best Local Similarity 26.6%; Pred. No. 1.4e-23;
 Matches 290; Conservative 129; Mismatches 308; Indels 364; Gaps 39;

Qy 134 PEDDEPPARPPPPPPASVSPQAE-PVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKI 192
 | : : | | | : | || || | : ||
 Db 5 PDLQDEPLSPANPGSQLFGGRGEGEEATPKGARPAQQDGEPAWGS--GAGAGVVS----- 57

Qy 193 MDLKEQPGNTISAGQEDFPSVLLETA----ASXP-SLSPLSAASFKEHE---YLGNLSTV 244
 : : | | : || | : | : | : | : | : | :
 Db 58 -----SRGLCSGPARSPPVAMETASTGVAAPDALDHSSSPTLKDGEACYTSLISDI 110

Qy 245 L--PTE-----GTLQE-----NVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFS 291
 | | | || : || : : : | : | | : | :
 Db 111 CYPRED SAYFTGILQKENGHITTSSESPEELGTPGPS-LPEVPGTEPHGLLSSDSGIEMT 169

Qy 292 VSPKAESAVIVANPREELIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSEKA 351
 : | | : : : : :
 Db 170 PAESTEVNKILADPLDQ----- 186

Qy 352 KDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCF 411
 | : | : | | : | | |
 Db 187 -----MKA EACKYIDITRQ EAKGQEEQSPGL----- 213

Qy 412 ADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATES--IATNIFPLL 469
 : || : : | : : || : || | : | | : | :
 Db 214 -----EDKDLDFKDKDSEVSTKPEGVH-----APNQPSPEVGKLIKDNLF--- 253

Qy 470 EDPTSENXTDEKKIEEKKAQIVTE--KNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527
 | : | | | : : : || | | : | | : :
 Db 254 EESTFAPYIDELSDEQHRMSLV TAPVKITLTEIGPPVMTATHET----- 297

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFE 587
 : || | | | | | : | : | :
 Db 298 ----IPE-----KQDL-----CLKPSPDTVPTVT 317

Qy 588 ESEA---TPSPVLPDIVMEAPLNSAVPSAGASVIQPS SSP-----LEASSVNYESIKH 637
 || : | | | : || | : | | | : : : :
 Db 318 VSEPEDDSPG SVTP-----PSSGTEPSAAESQKGKSVSEDELIAAIKEAKGLSYET--- 368

Qy 638 EPENPPPYEEAMSVSLKVGSIKEEIKE-----PENINAALQETEAPYISIIACDLIKET 690
 | : | | : | : : : | : : : | : | : : |

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ID      RTN1_HUMAN          STANDARD;          PRT;    776 AA.
AC      Q16799; Q16800; Q16801;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Reticulon 1 (Neuroendocrine-specific protein).
GN      RTN1 OR NSP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC      TISSUE=Lung carcinoma;
RX      MEDLINE=93293865; PubMed=7685762;
RA      Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V..

```

RA Ramaekers F.C.S., Van de Ven W.J.M.;
 RT "Cloning and expression of alternative transcripts of a novel
 RT neuroendocrine-specific gene and identification of its 135-kDa
 RT translational product.";
 RL J. Biol. Chem. 268:13439-13447(1993).
 RN [2]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96429995; PubMed=8833145;
 RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
 RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
 RT "Genomic organization of the human NSP gene, prototype of a novel gene
 RT family encoding reticulons.";
 RL Genomics 32:191-199(1996).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=98228245; PubMed=9560466;
 RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
 RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;
 RT "Neuronal differentiation is accompanied by NSP-C expression.";
 RL Cell Tissue Res. 292:229-237(1998).
 CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
 CC membrane trafficking in neuroendocrine cells.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=RTN1-A; Synonyms=NSP-A;
 CC IsoId=Q16799-1; Sequence=Displayed;
 CC Name=RTN1-B; Synonyms=NSP-B;
 CC IsoId=Q16799-2; Sequence=VSP_005644;
 CC Name=RTN1-C; Synonyms=NSP-C;
 CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
 CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; L10333; AAA59950.1; -.
 DR EMBL; L10334; AAA59951.1; -.
 DR EMBL; L10335; AAA59952.1; -.
 DR PIR; A46583; A46583.
 DR PIR; I60904; I60904.
 DR Genew; HGNC:10467; RTN1.
 DR MIM; 600865; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0030182; P:neuron differentiation; TAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Phosphorylation.
 FT TRANSMEM 603 623 POTENTIAL.
 FT TRANSMEM 726 746 POTENTIAL.
 FT DOMAIN 589 776 RETICULON.
 FT DOMAIN 609 612 POLY-LEU.
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).
 FT /FTId=VSP_005644.
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).
 FT /FTId=VSP_005645.
 FT VARSPLIC 569 588 GPGPLGPGAPPPLFLNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-C).
 FT /FTId=VSP_005646.
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 13.3%; Score 787.5; DB 1; Length 776;
 Best Local Similarity 31.9%; Pred. No. 2e-23;
 Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

Qy 588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQSSSSPLE---ASSVNY---- 632
 | ||| |||: : | |: | : : ||: | : |
 Db 141 EELGTPGPSLDPVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDIT 200
 Qy 633 --ESIKHEPENPPPYEEA-----MSVSLKVSIGIKEEIKEPENINAAL-----QET 675
 | :||: :: | |: :|| |::| | | : : : |
 Db 201 RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST 259
 Qy 676 EAPYISIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPVDHSELVED 722
 |||| || :| | ||: : : : | : : :
 Db 260 FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309
 Qy 723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF 761
 |||: | | || | : | || : :||:
 Db 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA----- 363
 Qy 762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821
 : || | : :| :| | || : : :
 Db 364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403
 Qy 822 TAVYSNDDLFISKEAQIRETETFSDSPIEIIIDFP---TLISSKTDSFS----- 868
 :: | | | ||: | | : | ||
 Db 404 SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP 444
 Qy 869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921
 : || : |: : | : : | : || | | | |
 Db 445 ASPSIQYSILREEREAEELDELIIESCDASSAS-----EESPKREQDSPPMKPSALD 496
 Qy 922 DF-----SKNGSATSKVLL-----LPPDVSA LGHTQAEIESIVKP 956
 | : | | | || | | | : : |
 Db 497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGAL-----EPETPMLP 551
 Qy 957 KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001
 : | : :||: | : | | : |||||
 Db 552 -----RKPEEDSSSNQSPAATKGGPLGPGAPPPLLF---LNKQKAIDL YWRDIK 599

CC reticulum (Potential).
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF195940; AAG31360.1; -.
 DR EMBL; BC014697; AAH14697.1; -.
 DR MGD; MGI:1339970; Rtn3.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 167 187 POTENTIAL.
 FT DOMAIN 49 237 RETICULON.
 SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

Query Match 10.6%; Score 626; DB 1; Length 237;
 Best Local Similarity 53.2%; Pred. No. 6.9e-18;
 Matches 125; Conservative 41; Mismatches 53; Indels 16; Gaps 4;

QY 960 EKEAEKKLPS-DTEKEDRSPSAIFSD-----LGKTS-----VVDLLYWRDIKKTG 1004
 | | : || : |||: || | | ||::|||:||||
 Db 3 ESSAATQSPSVSSSSSGAEPALGGGGSPGACPALGAKSCGSSCAVHDLIFWRDVKKTG 62
 QY 1005 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLE 1064
 ||| :| :||| ||::|| :| : |||||:||||:| |||:||||:||||:||||:
 Db 63 FVFGTTLIMLLSLAAFSVISVSYLILALLSVTISFRVYKSVIQAVQKSEEGHPFKAYLD 122
 QY 1065 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGL 1124
 :: :| | | |:: ||| :| : |||||:||||| || ||: ||||:||||:
 Db 123 VDTLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGAVFNGI 182
 QY 1125 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKA 1178
 ||||| : :||||:||||: |||||:| | | : ||||:| | : |||
 Db 183 TLLILAELLVFSVPVIEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIKAKKAE 237

RESULT 7

RTN3_HUMAN

ID RTN3_HUMAN STANDARD; PRT; 236 AA.

AC 095197;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
 DE protein II) (NSPLII).

GN RTN3 OR NSPL2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Retina;
 RX MEDLINE=99265974; PubMed=10331947;
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;
 RT "Cloning of a novel member of the reticulon gene family (RTN3): gene
 RT structure and chromosomal localization to 11q13.";
 RL Genomics 58:73-81(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
 RT "Cloning and expression analysis of a cDNA encoding a novel
 RT neuroendocrine-specific protein-like protein 1: NSPL1.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF059524; AAC99319.1; -.
 DR EMBL; AF059529; AAD20951.1; -.
 DR EMBL; AF059525; AAD20951.1; JOINED.

DR EMBL; AF059526; AAD20951.1; JOINED.
 DR EMBL; AF059527; AAD20951.1; JOINED.
 DR EMBL; AF059528; AAD20951.1; JOINED.
 DR EMBL; AF119297; AAD26810.1; -.
 DR EMBL; BC000634; AAH00634.1; -.
 DR EMBL; BC010556; AAH10556.1; -.
 DR EMBL; BC011394; AAH11394.1; -.
 DR EMBL; BC022993; AAH22993.1; -.
 DR Genew; HGNC:10469; RTN3.
 DR MIM; 604249; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT DOMAIN 48 236 RETICULON.
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCD7B7 CRC64;

Query Match 10.6%; Score 625.5; DB 1; Length 236;
 Best Local Similarity 54.8%; Pred. No. 7.1e-18;
 Matches 119; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

Qy 963 AEKKLPSTEDKEDRSPSAIFSAIDLKGTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022
 || | : : : ||::||:|||| ||| :| :|||| ||:
 Db 20 AEPSAPGGGGSPGACPALGTKSCSSSCAVHDLIFWRDVKKTGfVFGTTLIMLLSLAAFSV 79

 Qy 1023 VSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSAL 1082
 :|| :| : ||||| ||||| ||||:||||: ||: :| | | :|:
 Db 80 ISVVSYLILALLSVTISFRIYKSVIAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139

 Qy 1083 GHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYE 1142
 |:| :| : ||||:||||| || ||: ||||:||||: ||||| : :|||:|:
 Db 140 VHINRALKLIIRLFLVEDLVDLSKLAVFMWLMFTYVGAVFNGITLLILAEELLIFSVPIVYE 199

 Qy 1143 RHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178
 ::: ||||:|:| | : ||||:|:| | :|||
 Db 200 KYKTQIDHYVGIARDQTKSIVEKIQAKLPGIKKKAE 236

RESULT 8

RTN2_HUMAN

ID RTN2_HUMAN STANDARD; PRT; 545 AA.
 AC O75298; O60509;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPLI).
 DE protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

RC TISSUE=Lung carcinoma;
 RX MEDLINE=98360096; PubMed=9693037;
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
 RT "cDNA cloning, genomic organization, and expression of the human RTN2
 RT gene, a member of a gene family encoding reticulons.";
 RL Genomics 51:98-106(1998).
 RN [2]
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
 RC TISSUE=Brain;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression.";
 RL Mamm. Genome 9:274-282(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=RTN2-A;
 CC IsoId=O75298-1; Sequence=Displayed;
 CC Note=Isoform RTN2-C is produced by alternative initiation at
 CC Met-341 of isoform RTN2-A;
 CC Name=RTN2-B;
 CC IsoId=O75298-2; Sequence=VSP_005649;
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
 CC by alternative initiation at Met-1 and Met-341;
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
 CC MUSCLE.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF004222; AAC32542.1; -.
 DR EMBL; AF004223; AAC32543.1; -.
 DR EMBL; AF004224; AAC32544.1; -.
 DR EMBL; AF038540; AAC14910.1; -.
 DR Genew; HGNC:10468; RTN2.
 DR MIM; 603183; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Alternative initiation.
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.
 FT INIT MET 341 341 FOR ISOFORM RTN2-C.
 FT TRANSMEM 368 388 POTENTIAL.

FT TRANSMEM 463 483 POTENTIAL.
 FT DOMAIN 345 545 RETICULON.
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).
 FT /FTId=VSP_005649.
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 8.7%; Score 514; DB 1; Length 545;
 Best Local Similarity 28.2%; Pred. No. 3.7e-13;
 Matches 169; Conservative 81; Mismatches 186; Indels 164; Gaps 18;

Qy 676 EAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPD-SEPVDL-F 733
 ||| | | | | | : : : | | : | | : | |
 Db 13 EAP-----STASSTPDSTEGNDDSDFRELHTAREFSEEDDEE--ETTSQDWGTPRELTF 64

Qy 734 S-----DDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG 780
 | | | | | : | : | : | : | : | | | |
 Db 65 SYIAFDGVVGSGGRRDSTARPRPQGRSVSEPRDQHPQPSLGDLSLESIPSLSQSPEPGRR 124

Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840
 | | | | | | | | : | : : | : : : | |
 Db 125 GDP-----DTAPPSE----RPLEDLRLRLDHLG-----WVARGTGSGE 158

Qy 841 TETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 : | | : | | | | : | | | | | | | | | |
 Db 159 DSSTSSSTPLE--DEEP-----QEPNRLETGEAGE-----EL 188

Qy 901 PHDLSLKNIQPKVEEKI-----SFSDDFSKNGSATS KVL LPPDV SALGHT 946
 | | | : | | | : : | | : : : | | : |
 Db 189 --DLRLRLAQPS SPEVLTPQLSPGSGTPQAGTPSPSRSDSNSGPPEEPLLEEEEEKQWGPL 246

Qy 947 QAE-----IESIVKPKVLEKEAE-----KKLP----- 968
 : | : | | : | : | : | | : | : |
 Db 247 EREPVRGQCLDSTDQLEFTEPRLLGTAMEWLKTSLLLAVYKTVPILELSPPLWTAIGWV 306

Qy 969 -----SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASL 1011
 : : : | | | : | | | : | : | | | :
 Db 307 QRGPTPPTPVLRVLLKWAKSPRSSGVPSLSLGADMG-SKVADLLYWKDTRTSGVVFTGLM 365

Qy 1012 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071
 | | | | | | | | : : | | | | | : | : | : | : : :
 Db 366 VSLCLLHFSIVSVA AHLALLLLCGTISLRVYRKVLQAVHRGDGANPFQAYLDVDLTLTR 425

Qy 1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVILMWVFTYVGALENGLTLLILAL 1131
 | : : | : | : | | | : | | | : | : | : | : | : | : | :
 Db 426 EQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALLFYILT FVGAIENG LTLLILGV 485

Qy 1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-----KRKAE 1178
 | | : : | : | : | | | : | : | : | : | : | : | | | |
 Db 486 IGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAA VSGSKAKAE 545

RESULT 9

RTN2_MOUSE

ID RTN2_MOUSE STANDARD; PRT; 471 AA.

AC 070622; 070620;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
 DE protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression."
 RL Mamm. Genome 9:274-282(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Brain;
 CC IsoId=O70622-1; Sequence=Displayed;
 CC Name=2; Synonyms=Muscle;
 CC IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
 CC tissues.
 CC -!- SIMILARITY: Contains 1 reticulon domain.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

QY 1128 ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-----KR 1175
 || ::||:|:|:| :|:|:| |:| | : ||:|:|:| |
 Db 409 ILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGTLAPTASVSGSKA 468
 QY 1176 KAE 1178
 |||
 Db 469 KAE 471

RESULT 10

CPN_DROME

ID CPN_DROME STANDARD; PRT; 865 AA.
 AC Q02910;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calphotin.
 GN CPN OR CAP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=93165729; PubMed=8094559;
 RA Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
 RT "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=93165730; PubMed=8434015;
 RA Ballinger D.G., Xue N., Harshman K.D.;
 RT "A Drosophila photoreceptor cell-specific protein, calphotin, binds
 RT calcium and contains a leucine zipper.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
 CC -!- FUNCTION: Might function as a calcium-sequestering "sponge" to
 CC regulate the amount of free cytoplasmic calcium. It binds 0.3 mole
 CC of Ca(2+) per mole of protein.
 CC -!- SUBUNIT: Homodimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.
 CC -!- TISSUE SPECIFICITY: Soma and axons of photoreceptor cells of
 CC compound eyes and ocelli.
 CC -!- DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell
 CC development.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; L02111; AAA28405.1; -.
 DR EMBL; L05080; AAA28420.1; -.
 DR PIR; A47282; A47282.
 DR PIR; A47283; A47283.
 DR FlyBase; FBgn0010218; Cpn.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 KW Calcium-binding.
 FT CONFLICT 36 36 A -> AVAPAVVA (IN REF. 2).
 FT CONFLICT 43 43 I -> T (IN REF. 2).
 FT CONFLICT 64 64 I -> V (IN REF. 2).
 FT CONFLICT 76 76 T -> A (IN REF. 2).
 FT CONFLICT 100 100 P -> PP (IN REF. 2).
 FT CONFLICT 126 127 VQ -> AP (IN REF. 2).
 FT CONFLICT 154 154 I -> V (IN REF. 2).
 FT CONFLICT 160 160 S -> T (IN REF. 2).
 FT CONFLICT 534 534 A -> E (IN REF. 2).
 FT CONFLICT 699 699 I -> T (IN REF. 2).
 FT CONFLICT 703 703 V -> L (IN REF. 2).
 FT CONFLICT 721 721 D -> E (IN REF. 2).
 SQ SEQUENCE 865 AA; 84781 MW; 2110417E0B0E7CFE CRC64;

Query Match 5.5%; Score 324.5; DB 1; Length 865;
 Best Local Similarity 22.3%; Pred. No. 1.1e-05;
 Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGLPAAPPVAPERQPSWDPSPVSSSTVP 118
 | : |||| | | ||: | ||| |: | | | :| :|
 Db 9 PVSAPVAAPV-TPSAVAAPVQVWSPAAPVAPAAPIAVTPVAPPPTLASVQPATV--TIP 65

 Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPPAP----APAAPP--ST 172
 ||:|:|:|:|:| || | |||: || : || | || ||| :|
 Db 66 APAPIAAASVTP---VASVAPPVVAAPTTPAA--SPVSTPVAVAQIPVAVSAPVAPPVVAAT 121

 Qy 173 PAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF 232
 | : : |: | || |: || | :||: |:
 Db 122 PTPVVQIPVAAPVIAT-----PPVAASA-----PT----PAAVTPVISPVIAS-- 160

 Qy 233 KEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSV 292
 |:| | | |: : | :: | :|
 Db 161 -----PPVVPANTT---VPVAAPVAAPVAAVPVAPVLAP-----AV 194

 Qy 293 SPKAESAVIVAN-----PREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVS 347
 :| | :|| | || | :| : |:| ||:
 Db 195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVVA 234

 Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407
 : | : || | | | | | : : |: : : |
 Db 235 T---KPLAAAEPVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280

 Qy 408 KKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467
 || : : |:| || ||
 Db 281 -----ASTEPPV---AAATLTTPAPETPAL----- 301

 Qy 468 LLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527
 | :| | || | |
 Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579
 | | : | : | : | | : | | : | | : | | : | |
 Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371
 Qy 580 -AQLCPSEFESEATPSPVLDPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHE 638
 | | : : | : | | : : | : | | : | | : | | :
 Db 372 PATLAVTDPDVTASAVPELPPVIAVSPVPSAVAETPVDLAPPVLPPVAAEPVPAVVAEET 431
 Qy 639 PENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEP 697
 | | | | : : : | : : | | : | | : | | : : | |
 Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSADAPAEAPSAAPIVSTPPTTASVPETTAPPA 491
 Qy 698 P-----DFSDYSEMAKVEQVPVDHSEL-----VEDSSPDSEPVDLFSDD SIP--DVPQK 744
 | | | | : | | | : | | : | | : | | : | | :
 Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDL 550
 Qy 745 QDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEV 804
 : : | : | : : | : : | : : | : : : : |
 Db 551 LEQTTSPVAVEAAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603
 Qy 805 STLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLI 860
 | : | | : : : : | | : | | | | | | | :
 Db 604 SLATPTEPIPVVEAPVVIQEAVIDAV-----EVPVTETST---SIP-ETTVEFPEAV 649
 Qy 861 SSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDL SL 906
 : | | | : | : : : : | | | | | : | : : :
 Db 650 AEKV-----LDPAITEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701
 Qy 907 KNIQPKVEEKISFSDDFS KN GSATS KVL L-----LP-----PDVSALG----- 944
 | | | : : : : : : : : : : | | : | : |
 Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760
 Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLY 996
 : | | : | | : | | : | : : : | | | : | : |
 Db 761 ITAGDNPNTSVGISEVV-PTIAEKPVVEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814
 Qy 997 WRDIKKTGV 1005
 | | : | |
 Db 815 -RDLQTTDV 822

RESULT 11

PCLO_HUMAN

ID PCLO_HUMAN STANDARD; PRT; 5147 AA.
 AC Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Piccolo protein (Aczonin) (Fragments).
 GN PCLO OR ACZ OR KIAA0559.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-759 FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE=99439764; PubMed=10508862;
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
 RA Kilimann M.W.;
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
 RT zones, shares homology regions with rim and bassoon and binds
 RT profilin.";
 RL J. Cell Biol. 147:151-162(1999).
 RN [2]
 RP SEQUENCE OF 552-4404 FROM N.A.
 RA Kraemer J., Wollam C., Wohldmann P., McGrane B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 RN [4]
 RP SEQUENCE OF 4405-4439 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 4405-5147 FROM N.A.
 RA Kalicki J., Elliott G.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle
 CC trafficking (By similarity).
 CC -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
 CC synaptic junctions (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:

```

CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9Y6V0-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925,
CC      VSP_003926, VSP_003927;
CC      Note=No experimental confirmation available;
CC      -!- DOMAIN: C2 domain 1 is involved in binding calcium and
CC      phospholipids. Calcium binds with low affinity but with high
CC      specificity and induces a large conformational change.
CC      -!- SIMILARITY: Contains 2 C2 domains.
CC      -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y19188; CAB60727.1; -.
DR      EMBL; AC004903; AAD20936.1; -.
DR      EMBL; AC004886; AAD21789.1; -.
DR      EMBL; AB011131; BAA25485.1; -.
DR      EMBL; BC001304; AAH01304.1; -.
DR      EMBL; AC004082; AAB97937.1; -.
DR      PIR; T00634; T00634.
DR      HSSP; P04410; 1A25.
DR      Genew; HGNC:13406; PCLO.
DR      MIM; 604918; -.
DR      GO; GO:0005856; C:cytoskeleton; NAS.
DR      GO; GO:0045202; C:synaptic junction; ISS.
DR      GO; GO:0005509; F:calcium ion binding; ISS.
DR      GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
DR      GO; GO:0005522; F:profilin binding; ISS.
DR      GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR      GO; GO:0016080; P:synaptic vesicle targeting; ISS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001565; Synaptotagmin.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
KW      Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW      Repeat; Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      400      465      10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT                                     P-A-K-P-Q-P-Q-Q-P-X.
FT      ZN_FING      499      523      C4-TYPE (POTENTIAL).
FT      ZN_FING      969      992      C4-TYPE (POTENTIAL).
FT      NON_CONS     1010     1011
FT      DOMAIN      2300     2325      POLY-PRO.
FT      DOMAIN      4391     4442      PDZ.
FT      DOMAIN      4544     4633      C2 DOMAIN 1.

```

FT	DOMAIN	5031	5121	C2 DOMAIN 2.
FT	VARSPLIC	4404	4404	S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
FT				QTGKLMEG (in isoform 2).
FT				/FTId=VSP_003923.
FT	VARSPLIC	4534	4534	K -> KPTDGTKVVSHPITGEIQ (in isoform 2).
FT				/FTId=VSP_003924.
FT	VARSPLIC	4576	4576	G -> GQVMVQNAS (in isoform 2).
FT				/FTId=VSP_003925.
FT	VARSPLIC	4757	4761	TAHKS -> SKRRK (in isoform 2).
FT				/FTId=VSP_003926.
FT	VARSPLIC	4762	5147	Missing (in isoform 2).
FT				/FTId=VSP_003927.
SQ	SEQUENCE	5147 AA;	563537 MW;	CD5D84990498CD3C CRC64;

Query Match 5.4%; Score 320; DB 1; Length 5147;
 Best Local Similarity 21.8%; Pred. No. 0.00015;
 Matches 260; Conservative 152; Mismatches 440; Indels 340; Gaps 61;

Qy	8	PLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAP	67
		: : :	
Db	260	PSLPSPSKPPIQQPTPGKPPAQQPGHEKSQPG-----PAKPPAQPSGLT	303
Qy	68	VPTAPAAGA---PLMDFGNDFVPPAPRGPLPAAPPV-----	100
		:	
Db	304	KPLAQQPGTVKPPVQPPGTTKPPAQPLG--PAKPPAQQTGSEKPSSEQPGPKALAQPPGV	361
Qy	101	--APERQPSWDPSPVSVSTVPAPSPLS-----AAAVSPSKLPEDDEPPA-----RPP	144
		: : : : : :	
Db	362	GKTPAQQPG-PAKPPTQQVGTGPKPLAQQPLQSPAKAPGPTKTPAQTKPPSQQPGSTKPP	420
Qy	145	P--PPPASVSPQAEPVWTPPAPAP-AAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGN	201
		: : :	
Db	421	PQQPGPAKPSPPQPGSTKPPSQPGSAKPSA-----QQPSP	456
Qy	202	TISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKE	261
		: : : : : : :	
Db	457	AKPSAQQ-FTKPVSTGFGKPLQPPTVSPSAKQPPSQGLPKTICPL----CNTTELLH	510
Qy	262	VSEKA-----KTLII-----DRDLTEFSE-----LEYSEMGSFSVSPKA----	296
		: : : :	
Db	511	VPEKANFNTCTECQTTVCSLCGFNPNPHLTEAKEWLCCLNCQMKRALGGDLAPVPSSQPK	570
Qy	297	-----ESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQEL-----PTALTCLVKED	343
		: : : : :	
Db	571	LKTAPVTTTSAVSKSSPQPQQTSPKKDAAPK-----QDLSKAPEPKPPPLVKQP	620
Qy	344	EVVSSEKAK-----DSFNEKRVAVEAPMREE-----YADFKPFERVWEVKDSKEDSDM	391
		: : : : : :	
Db	621	TLHGSPSAKAKQPPEADSLSKPAPPKEPSVPSEQDKAPVADDKP----KQPKMVKPTTDL	676
Qy	392	LAAGGKIESNLESKVD---KKCFADSLEQTNHEKDSESSNDDTSFSTPEGIKDRSGAYI	448
		:: : : : : : : :	
Db	677	VSS-----SSATTKPDIPSSKVSQAEEKTTPPLKTDSAKPSQSFPPTGEKV-----	723
Qy	449	TCAPFN-----PAATESIATNIFPLLE-----DPTSENXTDEKKIEEKKAIQIVTEKN	495
		: : : :	
Db	724	--TPFDSKAIPRPASDSKIISHPGPSSESKGQKQVDPV-----QKKEEPKKAQTKMSPK	775

Qy 496 TSTK-----TSNPFFVAAQDSETDYVTDD-----NLTKVTEEVVANMPEGLT 537
 | | | | : | | : | : | : |
 Db 776 PDAKPMPKGSPTPPGPRPTAGQTVPTPQQSPKPKQEQSRRFSLNLGSITD---APKSQPTT 832
 Qy 538 PDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA--AQLCPSEFESEATPSP 595
 | || ||| : : | | : : | : | : | : | : | : |
 Db 833 P---QET-----VTGKLFGFGASI-FSQASNLISTAGQPGPHSQSGPGAPMKQA-PAP 880
 Qy 596 VLPDIVMEAPLNSA-VPSAGASVI-----QPSSSPLEASSVNYESIK--HEPENPPPY 645
 | : : | | | | : : | | : : | : | : | : |
 Db 881 SQPPTSQGPSTGQAPPAPAKSIPVKKETKAPAAEKLEPKAEQAPTVMKRTETETKPPPI 940
 Qy 646 EEAMSVSLKVSIGIKEEIKEPENINAALQETEAPYISIACDLIK-ETKLSAEPAPDFSDYS 704
 : : | : : || : : : : | | | | : : | : | : :
 Db 941 KDSKSLT-----AEPQKAVLPTKLEKSPKPESTCPLCKTELNIGSKDPNFTCT 990
 Qy 705 EMAKVE-----QVPDHSSELVE-----DSSPDSEPVDLFSDDS--- 737
 | | : | : | | : | : : : |
 Db 991 ECKNQVCNLCGFNPTPHLTENCQTQRAISGQLGDIRKMPPAPSGPKASMPVPTESSSQK 1050
 Qy 738 --IPDVPQ-----KQD-----ETVML--VKESLTETSFESMIEYENKEKLSALPPEGG 781
 : | || || : | : | | | : | : | : | : | :
 Db 1051 TAVP--PQVKLVKKQEVEKTEAEKVILEKVKETLSMEKIPPMVTTDQKQESKLEKDKA 1108
 Qy 782 KPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRET 841
 | | | | | : : | : : | | | : | : | : | :
 Db 1109 SALQE--KKPLPEEK-KLIPEE-EKIRSEEKKPLLEKKPTP----EDKLLPEAKTSAP 1160
 Qy 842 ETFSD---SSPIEIDE-FPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGA-GSLP 896
 | : : | : | : : || | : : : | | |||
 Db 1161 EEQKHDLKLSQVQIAEEKLEGRVAPKTVQEGK-----QPQTKMEGLPSGTPQSLP 1210
 Qy 897 CTELPHDLSLKNI-----QPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQ----- 947
 : | : | | || | : | : : | : | : | : :
 Db 1211 KED---DKTTKTIKEQPQPCTAKPDQEKEDDKSDTSSSQPKSPQGLSDTGYSSDGISS 1267
 Qy 948 --AEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGK--TSVVDLL 995
 || | : : || : | | | : : || : : | : | : | :
 Db 1268 SLGEIPSLIPTD--EKDILKGLKKDSFSQESSPSS--PSDLAKLESTVLSIL 1315

RESULT 12

PCLO_MOUSE

ID PCLO_MOUSE STANDARD; PRT; 5038 AA.
 AC Q9QYX7; Q9QYX6; Q9QZJ0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Piccolo protein (Presynaptic cytomatrix protein) (Aczonin) (Brain-
 DE derived HLMN protein).
 GN PCLO OR ACZ.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, ALTERNATIVE SPLICING,
 RP TISSUE SPECIFICITY, AND INTERACTION WITH PROFILIN.
 RC TISSUE=Brain;
 RX MEDLINE=99439764; PubMed=10508862;
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
 RA Kilimann M.W.;
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
 RT zones, shares homology regions with rim and bassoon and binds
 RT profilin.";
 RL J. Cell Biol. 147:151-162(1999).
 RN [2]
 RP REVISIONS.
 RA Kilimann M.W.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 4502-4682 FROM N.A.
 RC TISSUE=Brain;
 RA Huang W., Jin W., Huang C., Chen B., Zhang J., Ju G.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP INTERACTION WITH RIMS2.
 RX MEDLINE=22384373; PubMed=12401793;
 RA Fujimoto K., Shibasaki T., Yokoi N., Kashima Y., Matsumoto M.,
 RA Sasaki T., Tajima N., Iwanaga T., Seino S.;
 RT "Piccolo, a Ca2+ sensor in pancreatic beta-cells. Involvement of
 RT cAMP-GEFII.Rim2.Piccolo complex in cAMP-dependent exocytosis.";
 RL J. Biol. Chem. 277:50497-50502(2002).
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle
 CC trafficking.
 CC -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin.
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
 CC synaptic junctions.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9QYX7-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9QYX7-2; Sequence=VSP_003928, VSP_003929;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Low levels found in
 CC stomach. Not detected in other tissues analyzed including adrenal
 CC gland, testis and pancreas.
 CC -!- DOMAIN: C2 domain 1 is involved in binding calcium and
 CC phospholipids. Calcium binds with low affinity but with high
 CC specificity and induces a large conformational change.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -----
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 CC -----
 DR EMBL; Y19185; CAB60731.2; -.

DR EMBL; Y19186; CAB60732.2; -.
 DR EMBL; AF181269; AAD55786.2; -.
 DR HSSP; P04410; 1A25.
 DR MGD; MGI:1349390; Pclo.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0005509; F:calcium ion binding; ISS.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
 DR GO; GO:0005522; F:profilin binding; IDA.
 DR GO; GO:0019933; P:cAMP-mediated signaling; IDA.
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.
 DR GO; GO:0030073; P:insulin secretion; IDA.
 DR GO; GO:0017157; P:regulation of exocytosis; IDA.
 DR GO; GO:0016080; P:synaptic vesicle targeting; NAS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR008899; Znf_piccolo.
 DR Pfam; PF00168; C2; 2.
 DR Pfam; PF00595; PDZ; 1.
 DR Pfam; PF05715; Zf_piccolo; 2.
 DR SMART; SM00239; C2; 2.
 DR SMART; SM00228; PDZ; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 2.
 DR PROSITE; PS50106; PDZ; 1.
 KW Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;
 KW Repeat; Alternative splicing.
 FT DOMAIN 371 470 10 X 10 AA TANDEM APPROXIMATE REPEATS OF
 FT P-A-K-P-Q-P-Q-Q-P-X.
 FT ZN_FING 502 526 C4-TYPE (POTENTIAL).
 FT ZN_FING 967 990 C4-TYPE (POTENTIAL).
 FT DOMAIN 2305 2329 POLY-PRO.
 FT DOMAIN 4394 4488 PDZ.
 FT DOMAIN 4607 4705 C2 DOMAIN 1.
 FT DOMAIN 4922 5012 C2 DOMAIN 2.
 FT VARSPLIC 4829 4833 TKPTN -> SKRRK (in isoform 2).
 FT /FTId=VSP_003928.
 FT VARSPLIC 4834 5038 Missing (in isoform 2).
 FT /FTId=VSP_003929.
 SQ SEQUENCE 5038 AA; 547600 MW; DADA460CF3B40888 CRC64;

Query Match 5.3%; Score 315; DB 1; Length 5038;
 Best Local Similarity 22.0%; Pred. No. 0.00023;
 Matches 254; Conservative 136; Mismatches 435; Indels 328; Gaps 57;

Qy 57 RKPA--AGLSAAPVPTAPAAGAPLMDFG---NDFVPPAPR-----GPLPAAPPVAPE 103
 : || || :| | | | | : | :| | :|
 Db 288 KSPAQPAGTGKSPAQPPVTAKPPAQQAGLEKTSLQQPGPKSLAQTPGQGVPPGPAKSPA 347
 Qy 104 RQ-----PSWDPSP-VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ-A 155
 :| | :| | :| | | : | | | | :| | | ||
 Db 348 QQPGTAKLPAQQPGPQTASKVPGPTKTPAQLSGPGKTPAQQPGPTKPSQQPIPAKPQPQ 407
 Qy 156 EPVWT---PPAPAPAAPPP---STPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED 209
 :|| | | ||| | ||| : : : | | | | :
 Db 408 QPVATKPPQPPAPAKPQPQHPTPAKPQPQOPTPA-----KPQPQOPTPAKPQP 456
 Qy 210 FPSVLLETAASXPSLS-----PLSA--ASFKEHEYLGNLSTVLP---TEGTLQENV 256

Db	457	QHPGLGKPSAQQPSKISISQTVTGRPLQAPPTSAAQAPAQGLSKTICPLCNTTELLHTPE	516
Qy	257	EASKEVSEKAKTLLI-----DRDLTEFSEL-----EYSEMGSSFSVSPKA	296
Db	517	KANFNTCTECQSTVCSLCGFNPNPHLTEIKEWLCLNCQMQRALGGELAAIPSSPQPTPKA	576
Qy	297	ESAVIV-----ANPREEIIVKN---KDEEEK----LVSNNILHX-----QQE	331
Db	577	ASVQPATASKSPVPSQQASPKKELPSKQDSPKAPESKKPPPLVKQPTLHGPTPATAPQPP	636
Qy	332	LPTALTCLV--KEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS	389
Db	637	VAEALPKPAPPKKPSAALPEQAK-----APV----ADVEPKQP--KTETLTDS	679
Qy	390	DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYIT	449
Db	680	PSSAAATSKPAILSSQVQ---AQAVTTAPPLKTDSAKTSQSFPPTGD-----T	725
Qy	450	CAPFN-----PAATESIATNIFLLEDPTSENXTD-EKKIEEKKAQIVTEKNTSTKTSN	502
Db	726	ITPLDSKAMPRPASDSKIVSH-----PGPTSESKDPVQKKEPKKAQTKVTPKPDTK---	777
Qy	503	PFFVAAQDSETDYVTTDNLTKEEV-----VANMPEGLTPDLVQEACE	546
Db	778	PVPKGSPTPSGTRPTTGQATPQSQQPPKPPEQSRFSLNLGGIADAPKS-QPTTPQET--	834
Qy	547	SELNEVTGTKIAYETKMDLVQTEVMQESLYPAAQLCPSFEESEATPSPVLP---DIVM	602
Db	835	-----VTGKLFEGGASI-FSQASNLIS----TAGQQAPHPQTGPAAPSKQAPPPSQTLAA	884
Qy	603	EAPLNSA--VPSAGASVIQ-----PSSSPLEASSVNYESI-----KHEP---ENPP	643
Db	885	QGPPKSTGQHPSAPAKTTAVKKETKGPAAENLEAKPAQAPTVMKAEKDKKHPPGKVSPPP	944
Qy	644	PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISACDLIK-ETKLSAEPAPDFSD	702
Db	945	P-----TEPEKAVLAQKPDKTTKPKPACPLCRTELNVGSQDPPNFNT	986
Qy	703	YSEMAKVE-----QVPVDHSELVE-----DSSPDSEPVD	731
Db	987	CTECKNQVCNLCGFNPTPHLTEIQEWLCLNCQTQRAISGQLGDMDKMPPASSGPKASVVP	1046
Qy	732	LFSD-----DSIPDVPQKQDETV-----MLVKESLT	757
Db	1047	APAEPPPQKTPTAAHAKGKKKETEVKAETEKQIPEKETPSIEKTPPAVATDQKLESEVT	1106
Qy	758	ETSFESMIEYENKEKLSAL-----PPEGKPYLESFKLSLDNTKDTLLPDEVSTLSK	809
Db	1107	KSLVSVLPEKKPSEEEKALPADKKEKKPPAAEAPPLEEKKPIPDQK--LPPDAKPSASE	1164
Qy	810	KEKIPLQMEELSTAVYSNDDLFIKSAQIR-ETETFSDSPIEIIDFPTLISSKTDSFS	868
Db	1165	GEE---KRDLLKAHVQIPEEGPIKVASLACEGEQQPDTRPEDLPATPQTLPKD-----	1216
Qy	869	KLAREYTDLEVSHKSEIANAPDGAG--SLPCTELPHDLS--LKNIQPKVEEKISFSDDFS	924

Db 1217 ---RQKESRDVTQPQAEGTAKEGRGEPKDRTEKEEDKSDTSSSSQQPKSPQGLS-DTGYS 1272
 Qy 925 KNGSATSKVLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSA 984
 Db 1273 SDGISGS-----LG----EIPSLIPSD--EKDLLKGLKKDSFSQESSPSS--PS 1313
 Qy 985 DLGK--TSVVDLL 995
 Db 1314 DLAKLESTVLSIL 1326

RESULT 13

ANK2_HUMAN

ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
 AC Q01484; Q01485;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain stem;
 RX MEDLINE=91302466; PubMed=1830053;
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RT "Isolation and characterization of cDNAs encoding human brain
 RT ankyrins reveal a family of alternatively spliced genes.";
 RL J. Cell Biol. 114:241-253(1991).
 RN [2]
 RP REVISIONS.
 RA Carpenter S.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain stem;
 RX MEDLINE=94075409; PubMed=8253844;
 RA Chan W., Kordeli E., Bennett V.;
 RT "440-kD ankyrinB: structure of the major developmentally regulated
 RT domain and selective localization in unmyelinated axons.";
 RL J. Cell Biol. 123:1463-1473(1993).
 RN [4]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE=92009921; PubMed=1833308;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 RT ankyrin gene.";
 RL Genomics 10:858-866(1991).
 CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
 CC elements. Also bind to cytoskeletal proteins.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;

```

CC      IsoId=Q01484-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
CC      Name=3;
CC      IsoId=Q01484-3; Sequence=VSP_000268;
CC      -!- TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial
CC          cells throughout the brain.
CC      -!- PTM: Phosphorylated at multiple sites by different protein kinases
CC          and each phosphorylation event regulates the protein's structure
CC          and function (Potential).
CC      -!- SIMILARITY: Contains 23 ANK repeats.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -----
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CC      -----
DR      EMBL; X56957; CAA40278.1; -.
DR      EMBL; X56958; CAA40279.2; -.
DR      EMBL; Z26634; CAB42644.1; -.
DR      EMBL; M37123; AAA62828.1; -.
DR      PIR; S37431; S37431.
DR      HSSP; P42771; 1DC2.
DR      Genew; HGNC:493; ANK2.
DR      MIM; 106410; -.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00023; ank; 24.
DR      Pfam; PF00531; death; 1.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      SMART; SM00248; ANK; 22.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50088; ANK_REPEAT; 20.
DR      PROSITE; PS50297; ANK_REP_REGION; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
KW      Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW      Phosphorylation.
FT      REPEAT      63      92      ANK 1.
FT      REPEAT      96      125     ANK 2.
FT      REPEAT     129      158     ANK 3.
FT      REPEAT     162      191     ANK 4.
FT      REPEAT     193      220     ANK 5.
FT      REPEAT     232      261     ANK 6.
FT      REPEAT     265      294     ANK 7.
FT      REPEAT     298      327     ANK 8.
FT      REPEAT     331      360     ANK 9.
FT      REPEAT     364      393     ANK 10.
FT      REPEAT     397      426     ANK 11.
FT      REPEAT     430      459     ANK 12.
FT      REPEAT     463      492     ANK 13.

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FT	REPEAT	496	525	ANK 14.
FT	REPEAT	529	558	ANK 15.
FT	REPEAT	562	591	ANK 16.
FT	REPEAT	595	624	ANK 17.
FT	REPEAT	628	657	ANK 18.
FT	REPEAT	661	690	ANK 19.
FT	REPEAT	694	723	ANK 20.
FT	REPEAT	727	756	ANK 21.
FT	REPEAT	760	789	ANK 22.
FT	REPEAT	793	822	ANK 23.
FT	DOMAIN	1773	1950	REPEAT-RICH REGION.
FT	REPEAT	1773	1784	REPEAT A.
FT	REPEAT	1785	1796	REPEAT A.
FT	REPEAT	1797	1808	REPEAT A.
FT	REPEAT	1809	1820	REPEAT A.
FT	REPEAT	1821	1832	REPEAT A.
FT	REPEAT	1833	1844	REPEAT A.
FT	REPEAT	1845	1856	REPEAT A.
FT	REPEAT	1857	1867	REPEAT A (APPROXIMATE).
FT	REPEAT	1868	1879	REPEAT A.
FT	REPEAT	1880	1891	REPEAT A.
FT	REPEAT	1892	1902	REPEAT A (APPROXIMATE).
FT	REPEAT	1903	1914	REPEAT A.
FT	REPEAT	1915	1926	REPEAT A.
FT	REPEAT	1927	1938	REPEAT A.
FT	REPEAT	1939	1950	REPEAT A.
FT	DOMAIN	3536	3620	DEATH.
FT	VARSPPLIC	1039	1039	Q -> QFLGKLHLPTAPPPLNEGESLVSRIQLGPPGTK
FT				(in isoform 2).
FT				/FTId=VSP_000267.
FT	VARSPPLIC	1444	3528	Missing (in isoform 2 and isoform 3).
FT				/FTId=VSP_000268.
FT	CONFLICT	475	476	GQ -> PE (IN REF. 4).
FT	CONFLICT	971	971	I -> S (IN REF. 1).
FT	CONFLICT	3581	3582	QY -> HA (IN REF. 1).
FT	CONFLICT	3586	3586	I -> Y (IN REF. 1).
SQ	SEQUENCE	3924	AA; 430337 MW; 52AC496C428E29D2 CRC64;	

Query Match 5.0%; Score 299; DB 1; Length 3924;
 Best Local Similarity 21.5%; Pred. No. 0.00069;
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

QY	14	DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK	58
		: : : : : : :	
Db	1648	DIPPDDETQSTQKQHKPSLGIKKPVRRKLKEKQKQKEEGLQASAEKAEKKGSSEESLGED	1707
QY	59	PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----	92
		: : : ::: : :	
Db	1708	P--GLAPEPLPTVKAT-SPLIEETPIGSIKDKVKALQKRVEDEQKGRSKLPPIRVKGKEDV	1764
QY	93	-----PLPAA-PPVAPERQPSWDPSP-----VSSTVPAPSPL	123
		:	
Db	1765	PKKTTHRPHPAASPSLKERHAFGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV	1824
QY	124	SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW	159
		: : : : :	
Db	1825	SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSTKTERHPPVSPSGKTDKRPPV-	1883

Qy	160	TPPAPAPAAPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLE	216
Db	1884	SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLPVSPSG	1934
Qy	217	TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT	268
Db	1935	KTEKQPPVSPTS KTERIEETMSVRELMAKAFQSGQDPSKHKTGLFEHKSQKQKQPEKGKV	1994
Qy	269	-----LLIDRDLTEFSELEYSEMSSFSVSPKAES--AVIVANPREEIIVKNKDE--	316
Db	1995	RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAESKRGVRVSS----IGVKKEDAAG	2049
Qy	317	-EEKLVSNNI-----LHXQQELPTALTCLVKE-----DEVV	346
Db	2050	GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGDMDLQISPDRTSTDFSEVI	2107
Qy	347	SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED-----	388
Db	2108	KQLEDNDKYQQFRLSEETEKALHLQVLTSPFNTTFPLDYMKDEFLPALSLQSGALDG	2167
Qy	389	-SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDSESSNDDTSFPSTPEGIKDRS	444
Db	2168	SSESLKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT	2225
Qy	445	GAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPF	504
Db	2226	G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTEDSETSTESFQKE	2277
Qy	505	FVAAQDSETDYVTTDNLTKVTEEVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKM	563
Db	2278	ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT---EEAACDEGQRTFGSS-AHKT--	2330
Qy	564	DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVL-----PDIVMEAP--LNSAV	610
Db	2331	---QTDSEAQES-----TATSDETKALPLPEASVKTDGTESKPGQGVIRSPQGLELAL	2380
Qy	611	PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVS	657
Db	2381	PSRDSEVL SAVADDSLAVSHKDSLEASPVLEDNSSHKTPDSLEPSPLKESPCRDSLESSP	2440
Qy	658	IKEEIKE---PEN--INAALQETE--APYISIACDLIKETKLSAEPAPDFSDYSEMAKVE	710
Db	2441	VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE	2490
Qy	711	QPVPDHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	765
Db	2491	Q-----TSLMESSGKSPLSPDTPSSEEVSYEVT PKTTDVSTPKPAVIHECAEED-----	2539
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK---EKIPLQMEELS	821
Db	2540	DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAKQKRDKPEKQEESSS	2589
Qy	822	TAVYSNDDLFISKEA-QIRETETFSDDSPIEIIDFPTLISSKTDSFSKLAREYTDLEVS	880
Db	2590	S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSES RKVSSSSS-----	2633

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QY      881 HKSEIANAPDGAGS-----LPCTELPHDLSLKN-----IQPKVEEKISF--SDD 922
      : |:|   || |   | : || :   :   || | :: :| ::|
Db      2634 -EPQLAQLKKGADSGLLPEPVIRVQPPSPPLSSMDSNSSPEEVQFQPVVSKQYTFKMNE 2692

QY      923 FSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPD-----TEKEDRS 977
      :   : :   ||::| | |   || |||
Db      2693 TQEEPGKSEE-----EKDSESHLAEDRHAVSTEAEDRS 2725

```

RESULT 14

MAPB_HUMAN

```

ID      MAPB_HUMAN      STANDARD;      PRT; 2468 AA.
AC      P46821;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
DE      LC1].
GN      MAP1B.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Fetal brain;
RX      MEDLINE=95104835; PubMed=7806212;
RA      Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
RT      "Cloning of human microtubule-associated protein 1B and the
RT      identification of a related gene on chromosome 15.";
RL      Genomics 22:273-280(1994).
CC      -!- FUNCTION: The function of brain MAPS is essentially unknown.
CC      Phosphorylated MAP1B may play a role in the cytoskeletal changes
CC      that accompany neurite extension. Possibly MAP1B Binds to at least
CC      two tubulin subunits in the polymer, and this bridging of subunits
CC      might be involved in nucleating microtubule polymerization and in
CC      stabilizing microtubules.
CC      -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
CC      with MAP1A and MAP1B proteins.
CC      -!- DOMAIN: Has a highly basic region with many copies of the sequence
CC      KKEE and KKEI/V, repeated but not at fixed intervals, which is
CC      responsible for the binding of MAP1B to microtubules.
CC      -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
CC      from MAP1B by proteolytic processing. It is free to associate with
CC      both MAP1A and MAP1B. It interacts with the amino-terminal region
CC      of MAP1B (By similarity).
CC      -!- SIMILARITY: TO MAP1A.
CC      -----
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CC      -----
DR      EMBL; L06237; AAA18904.1; -.

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DR Genew; HGNC:6836; MAP1B.
 DR MIM; 157129; -.
 DR GO; GO:0005875; C:microtubule associated complex; TAS.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 6.
 KW Microtubule; Repeat; Phosphorylation.
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1878 1894 MAP1B 1.
 FT REPEAT 1895 1911 MAP1B 2.
 FT REPEAT 1912 1928 MAP1B 3.
 FT REPEAT 1929 1945 MAP1B 4.
 FT REPEAT 1946 1962 MAP1B 5.
 FT REPEAT 1963 1979 MAP1B 6.
 FT REPEAT 1997 2013 MAP1B 7.
 FT REPEAT 2014 2030 MAP1B 8.
 FT REPEAT 2031 2047 MAP1B 9.
 FT REPEAT 2048 2064 MAP1B 10.
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 5.0%; Score 296.5; DB 1; Length 2468;
 Best Local Similarity 21.5%; Pred. No. 0.00049;
 Matches 264; Conservative 148; Mismatches 459; Indels 355; Gaps 59;

Qy 2 EDLDQSPVLVSSS-DSPRPQPAFKYQ---FVREP-----EDEE 35
 || :: ||:| || : : | : :|| | :
 Db 956 EDGEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGEAEQ 1015

 Qy 36 EEEEEEEDEDEDLEEELEV-LERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPL 94
 ||| :|||: || | | |: | | | | | :| | |
 Db 1016 SEEEADEEDKAEDAREEEYEPEKMEAEDYVMAVVDKAAEAGGAEQYGFLLTPTKQLG-- 1073

 Qy 95 PAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ 154
 :| |:|: | |:| | | | |:| | | :
 Db 1074 ----AQSPGREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTATSGYT 1120

 Qy 155 AEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----D 209
 : | | | | | :| : | | |
 Db 1121 QSTIEISSEPTPMDEMSTP-----RDVMSDETNNETESPSQEFVNITK 1164

 Qy 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259
 : | | | |: :||: | | :| : ||: | : : | : :
 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFERSA 1222

 Qy 260 -----KEVSEKAKTLLIDRDLTEF-----SELEYSEMGS---SFS 291
 || || | | :| | | : :| :||
 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPSKSPSLSPSPSPLEKTPLGERSVNF 1280

 Qy 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328
 :| | | :| :| :|: : : | :| : : |
 Db 1281 LTPNEIKVSAEAEVAPVSPEVTQEVVEEHCASPEDKTLEVVSQSVTGSAGHTPYQSP 1340

 Qy 329 ----QQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383
 ||| : : | | : | : : | :|| | : | | :|
 Db 1341 TDEKSSHLPTEV--IEKPPAVPVSFESDAKDENERASVSPMDEPVPDSESPIEKVLSP 1398

Qy 384 DSKEDSDMLAAGGKIESNLESKVDKKCFADSLQTNHEKDSSESSNDDTSFPSTPEGIKDR 443
 | : : | | : | | | : : | :
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEKSGKQSPDQVSPVSE----- 1447

Qy 444 SGAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKK-----IEKK-----A 488
 : | : : | : | | : : : : :
 Db 1448 ----MTSTSLYQDKQEGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSP 1503

Qy 489 QI-----VTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVA--N 531
 || : : | : | : | : : : :
 Db 1504 QIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDTYSHMEGVASVSTASVATSS 1561

Qy 532 MPEGLTPDLVQEACESELNEVTGKTIAYETKMDLVQTSEVMQES-LYPAAQLCP----- 584
 || | | : : : : : : : : : :
 Db 1562 FPEPTTDD-VSPSLHAEVGSPPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRMSIS 1620

Qy 585 -----SFESEATPSPVLP-DIVMEAPLNSAVPSAGASVI 618
 | : : | | : : | : || :
 Db 1621 PPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPDH---PTVGAGVL 1677

Qy 619 Q-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSGIKEEIKE 664
 | : | : | : | : | : || : :
 Db 1678 HITENGPTVDYSPSDMQDSSLSHKIPMEEPSYTQDNDLSELISVSQVEASPSTSSAHT 1737

Qy 665 PENINAALQETE----AP-----YISIACDLIKE---TKLSAEP-----A 697
 | | : || | | : : : : : :
 Db 1738 PSQIASPLQEDTLSDVAPPRDMSLYASLTSEKVQSLEGEKLSPKSDISPLTPRESSPLYS 1797

Qy 698 PDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS----- 734
 | || : | : | | | : |
 Db 1798 PTFSDSTSAVK-EKTATCHS----SSSP---PIDAASAEPYGFRAVLFDTMQHHLALNR 1849

Qy 735 DDSIPDVP-----QKQDETVM LVKESLTETSFESMIEYENKEKLSALPPE 779
 | | : : || : || | : | : || :
 Db 1850 DLSTPGLEKDSGGKTPGDFSYAYQKPEET-----TRSPDEEDYDYESYEKTTTRTSDV 1901

Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKEAQIR 839
 || | : : : | : | : | | : | :
 Db 1902 GGY-YYEKIERTTKSPSDSGYSYE--TIGKTTKTP-----EDGDYSYE--IEKTTTRTP 1950

Qy 840 ETETFSDSPIEIIIDEFPTLISSKTDs---FSKLAREYTDLEVSHKSEIANAPDGAGSLP 896
 | : | | | | : | : : : :
 Db 1951 EEGGYSYD-----ISEKTTSPPEVSGYSYEKTERSRRLLDDISNGYDDS---- 1994

Qy 897 CTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAE-IESIVK 955
 : | | : : || : : || | : || :
 Db 1995 -EDGGHTLGDPSSYSYETTEKITSFPESEGYSYETSTKTTTRTPDTSTYCYETAEKITRTPQ 2053

Qy 956 PKVLEKE-----AEKKLPSDTEKE 974
 | ||| || : :
 Db 2054 ASTYSYETSDLCYTAEKKSPSEARQD 2079

RESULT 15

MAPB_RAT

ID MAPB_RAT

STANDARD;

PRT; 2459 AA.

AC P15205; Q62958; Q9ER21; Q9QW92;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
 DE light chain LC1].
 GN MAP1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-142 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=96257242; PubMed=8666295;
 RA Liu D., Fischer I.;
 RT "Isolation and sequencing of the 5' end of the rat microtubule-
 RT associated protein (MAP1B)-encoding cDNA.";
 RL Gene 172:307-308(1996).
 RN [2]
 RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;
 RX MEDLINE=92347374; PubMed=1639092;
 RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
 RT "Identification of two distinct microtubule binding domains on
 RT recombinant rat MAP 1B.";
 RL Eur. J. Cell Biol. 57:66-74(1992).
 RN [3]
 RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Spinal cord;
 RX MEDLINE=90059871; PubMed=2555150;
 RA Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
 RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
 RT "Neuraxin, a novel putative structural protein of the rat central
 RT nervous system that is immunologically related to microtubule-
 RT associated protein 5.";
 RL EMBO J. 8:2879-2888(1989).
 RN [4]
 RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
 RX MEDLINE=97405699; PubMed=9260743;
 RA Ma D., Nothias F., Boyne L.J., Fischer I.;
 RT "Differential regulation of microtubule-associated protein 1B (MAP1B)
 RT in rat CNS and PNS during development.";
 RL J. Neurosci. Res. 49:319-332(1997).
 CC -!- FUNCTION: The function of brain MAPS is essentially unknown.
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes
 CC that accompany neurite extension. Possibly MAP1B Binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
 CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
 CC heart or muscle.
 CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
 CC nerve levels are high early in development but decrease during

CC postnatal development and are low in adults. In dorsal root
 CC ganglia levels remain high throughout development.
 CC -!- INDUCTION: By nerve growth factor.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (By similarity).
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: TO MAP1A.
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to
 CC 2459) was originally described as neuraxin in Ref.3.

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DR EMBL; U52950; AAB17068.1; -.
 DR EMBL; X60370; CAC16162.1; -.
 DR EMBL; X16623; CAA34620.1; ALT_SEQ.
 DR PIR; A56577; A56577.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 8.
 KW Microtubule; Repeat; Phosphorylation.

FT	CHAIN	?	2459	MAP1 LIGHT CHAIN LC1.
FT	REPEAT	1869	1885	MAP1B 1.
FT	REPEAT	1886	1902	MAP1B 2.
FT	REPEAT	1903	1919	MAP1B 3.
FT	REPEAT	1920	1936	MAP1B 4.
FT	REPEAT	1937	1953	MAP1B 5.
FT	REPEAT	1954	1970	MAP1B 6.
FT	REPEAT	1988	2004	MAP1B 7.
FT	REPEAT	2005	2021	MAP1B 8.
FT	REPEAT	2022	2038	MAP1B 9.
FT	REPEAT	2039	2055	MAP1B 10.
FT	DOMAIN	559	1035	GLU-RICH.
FT	DOMAIN	588	786	LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
FT	DOMAIN	2224	2312	LYS-RICH.
FT	CONFLICT	127	127	M -> V (IN REF. 1).
FT	CONFLICT	140	140	T -> S (IN REF. 1).
FT	CONFLICT	2112	2112	R -> K (IN REF. 3).
FT	CONFLICT	2169	2169	L -> I (IN REF. 3).
SQ	SEQUENCE	2459	AA; 269497	MW; 2E3F6872DEDB8BA2 CRC64;

Query Match 4.9%; Score 289; DB 1; Length 2459;
 Best Local Similarity 20.9%; Pred. No. 0.00094;
 Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

Qy 30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFFVPPA 89

Db	1004	EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDKAAEAGVTEDQY--DFL---	1058
Qy	90	PRGPLPAAPP--VAPERQPSWDPSVPSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP	147
Db	1059	---GTPAKQPGVQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEF	1106
Qy	148	PASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ	207
Db	1107	TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNEEETESPSQ	1150
Qy	208	E-----DFPSVLLETAASXP---SLSPLSAASFKE----HEYLGNLSTVLPTEGTLQENV	255
Db	1151	E FVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEEDKF	1210
Qy	256	SEAS-----KEVSEK-----AKTLLIDRDLTE	277
Db	1211	SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPSPIEKTPLGERSV-N	1269
Qy	278	FS----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIVKNK-----	314
Db	1270	FSLTPNEIKASAEGEATAVSPGVTQAVVEHCASPEEKTLEVVSPSQSVTGSAGHTPY	1329
Qy	315	----DEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSE--KAKDSFNEKRVAVEAPMRE	368
Db	1330	QSPTDEKSSHLPTVETENAQAVP-----VSFEFTEAKDE-NER--SSISPMDE	1374
Qy	369	EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDKKCFADSL	415
Db	1375	PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPFEGKNGKQGFSD--	1432
Qy	416	EQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNP---AATESIATNIFPILLED-	471
Db	1433	-----KESPVS-DLTSDLYQDKQEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE	1485
Qy	472	-----PTSENXTDEKKIEEKKAIQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTK	523
Db	1486	RKLGGDGSPQTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS	1542
Qy	524	VTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES-LYPAA	580
Db	1543	VSTASVATSSFPPTTDD-VSPSLHAEVGSHPSTEVDDSLSVSVVQTPPTTFQETEMSPSK	1601
Qy	581	QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P	611
Db	1602	EECPRMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHP	1661
Qy	612	SAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG	657
Db	1662	TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPTEEPSYTDNDLSELISVSQVEASP	1721
Qy	658	IKEEIKEPENINAALQETE-----APYISACDLIKE---TKLSAEP-----	696
Db	1722	STSSAHTPSQIASPLQEDTLSDVPPRDMSLYASLASEKVQSLEGEKLSPKSDISPLTPR	1781
Qy	697	-----APDFSDYSEMAK-----VEQPVPDHSELVEDS-----	723

Db 1782 ESSPTYSPGFSDSTSGAKESTAAYQTSSSPIDAAAAEPYGFRSSMLFDTMQHHLALS RD 1841
 Qy 724 -----SPDSEPVDLFSDD---SIPDVP----QKQD 746
 ||| | | | : || :| :
 Db 1842 LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYEYKTE 1901
 Qy 747 ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD 797
 |: | |:| : | || : | ||| | : ::
 Db 1902 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTRTPEEGGYSY-----EISEK 1953
 Qy 798 TLLPDEVs--TLskKEIPLQMEELSTAVYSNDD-----LFISKEA 836
 | ||| | | |: ::::| :| | :
 Db 1954 TTRTPEVSGYTYEKTERSRRLLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 2013
 Qy 837 QIRETETFSdSSP-----IEIIDEFPTLISSKTDsFSKLAREYT-----DL 877
 || | : || | :: : | |: | || ||
 Db 2014 YSYETTTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 2073
 Qy 878 -----EVSH-KSEIANA---PDG---AGSLPCTELPHDLsLKNIQP-----KV 913
 | | |:|: : | : || | | | : | :
 Db 2074 CLVSSCEFKHPKTELSPSFINPNPLEWFAGEEPTeESERPLTQSGGAPPPSGGKQQGRQC 2133
 Qy 914 EEKISFSDDFSKNGSATSsKVLllPPDVSA LGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970
 :| | | | | ||: | || |: | | : :|:|
 Db 2134 DETPPTSVSESAPSQTDSdV---PPETE-----ECPSITADANLDSEDESEtIPTDKT 2183
 Qy 971 -----TEKEDRSPS-----AIFsADLGKTSVVDLLYWRDIKKTG 1004
 :|||| | :|| | | |||
 Db 2184 VTYKHMDPPPAPMQDRSPSPRHPDVSMVDPEALAIEQNLGKALKKDLKEKAKTKKPG 2240

Search completed: September 3, 2004, 16:06:11
 Job time : 24.6624 secs